

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2005, 10:35:37 ; Search time 13.1953 Seconds
(without alignments)

9421.101 Million cell updates/sec

Title: US-10-764-075-2

Perfect score: 21
Sequence: 1 atgaccacacaaggcagatgg 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	29751	12	ADJ39000 SARS CO
2	17.8	84.8	1560	6	ABV78222 Human MMP
3	17.8	84.8	1560	6	ABZ35798 Human MMP
4	17.8	84.8	1560	6	ABX10041 Human MMP
5	17.8	84.8	1560	6	ABL91763 Human pol
6	17.8	84.8	1818	6	ABV78191 Human MT4
7	17.8	84.8	1818	6	ABZ35767 Human MT4
8	17.8	84.8	1818	6	ABX10010 Human MT4
9	17.8	84.8	1818	6	ABL91732 Human pol
10	17.8	84.8	2295	3	AAAL3389 Human MT4
11	17.8	84.8	2295	3	AAAL4351 Human MT4
12	17.8	84.8	2306	10	AAH28234 Nucleotid
13	17.8	84.8	2306	10	AD884832 Farnesyl
14	17.8	84.8	2423	3	AAAL4340 cDNA enco
15	17.8	84.8	2423	8	ABZ20920 MT4-WMP c
16	17.8	84.8	2438	3	AAAL3377 Human MT4
17	17.8	84.8	2438	10	ACF63409 Human MMP
18	17.8	84.8	2438	12	ADK14165 Human aut
19	17.8	84.8	2438	12	AD028632 Human MMP
20	17.8	84.8	2438	12	ADQ19326 Human sof

21	17.8	84.8	3007	12	ADQ23578 Human sof
22	17.4	82.9	3003	11	ADM01725 Human CDN
23	17.4	82.9	6952	10	ADL24806 Intestina
C 24	16.8	80.0	74	10	ACD95453 Human col
C 25	16.8	80.0	74	10	ACD93726 Human col
C 26	16.8	80.0	224	10	ABX88992 Corn ear-
27	16.8	80.0	270	6	ABV96477 Human pan
28	16.8	80.0	415	2	AAK30910 Streptoco
C 29	16.8	80.0	451	10	ADD71720 Human uri
30	16.8	80.0	487	2	AZ96487 S. pneumo
31	16.8	80.0	630	13	ADQ57025 Novel can
32	16.8	80.0	890	10	ABX07482 S. pneumo
33	16.8	80.0	891	12	ADM91971 S. pneumon
34	16.8	80.0	894	4	AA855733 Streptoco
35	16.8	80.0	894	8	ACA50075 Prokaryot
C 36	16.8	80.0	978	10	ADD71721 Human uri
37	16.8	80.0	1222	3	AA859283 Human sec
38	16.8	80.0	1323	3	AA81772 Human bea
39	16.8	80.0	1446	12	ADO07809 Human pol
C 40	16.8	80.0	1792	10	ADD71722 Human uri
41	16.8	80.0	1792	12	ADL26142 Human CDN
42	16.8	80.0	1814	13	ADP24393 PRO polyP
43	16.8	80.0	2354	6	AAU32038 Human kin
44	16.8	80.0	2446	2	AA89852 Human pro
45	16.8	80.0	2488	4	AA44675 Novel pro

ALIGNMENTS

RESULT 1

ADJ39000
ID ADJ39000 standard; DNA; 29751 BP.
XX
AC ADJ39000;
XX
DT 06-MAY-2004 (first entry)
XX
DE SARS coronavirus nucleotide sequence.
XX
KW small interfering RNA; siRNA; modified ribonucleotide;
KW viral replication inhibition; hepatitis C virus; HCV; hepatitis C;
KW antiinflammatory; hepatotropic; virucide; hepatitis A virus;
KW hepatitis D virus; hepatitis E virus; Ebola virus; influenza virus;
KW rotavirus; reovirus; retrovirus; poliovirus; human papilloma virus;
KW metapneumovirus; coronavirus; viral infection; gene; ds.
XX
OS SARS coronavirus.
XX
PN WO2004011647-A1.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023104.
XX
PR 26-JUL-2002; 2002US-0398605P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Han J, Seo MY, Houghton M;
XX
DR WPI; 2004-143862/14.
XX
PT New RNase resistant small interfering RNA, useful for treating viral
PT infections, e.g., hepatitis C, influenza virus or coronavirus infection.
XX
PS Example 10; Fig 3; 74pp; English.
XX
CC The present invention describes a small interfering RNA (siRNA) which
CC comprises a modified ribonucleotide, where the siRNA is resistant to
CC RNase and retains the ability to inhibit viral replication. Also
CC described: (1) inactivating a virus in a patient; (2) making a modified
CC siRNA that targets a nucleic acid sequence in a virus; (3) a double-

stranded RNA molecule of 10-30 nucleotides that inhibits replication of hepatitis C virus (HCV); (4) inducing targeted RNA interference toward HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector comprising a DNA segment encoding the RNA molecule; (7) a host cell carrying the vector of (6); (8) inhibiting replication of HCV in cells carrying HCV; (9) treating hepatitis C in a subject; (10) a modified siRNA molecule comprising a double-stranded RNA molecule of 10-30 nucleotides in length, which mediates RNA interference toward a target agent or virus and is linked to at least one receptor-binding ligand; and (11) inducing targeted RNA interference in a patient. The modified siRNA molecule have antiinflammatory, hepatotropic and virucide activities. The modified RNA molecules are useful for inactivating virus in mammalian cells. The siRNAs are useful for treating hepatitis C virus, hepatitis A virus, hepatitis D virus, hepatitis E virus, Ebola virus, influenza virus, rotavirus, reovirus, retrovirus, poliovirus, human papilloma virus, metapneumovirus or coronavirus infections. The methods of the invention can be used to correct or compensate for cellular physiological abnormalities involved in conferring susceptibility to viral infections in patients and/or alleviate symptoms of a viral infection in patients. The present sequence represents the SARS coronavirus nucleotide sequence, which is used in an example from the present invention.

Sequence 29751 BP; 8478 A; 5941 C; 6188 G; 9144 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 12; Length 29751;
Best Local Similarity 100.0%; Pred. No. 3.4; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 ATGACCACACAGGCGAGTGG 21
|||||
DB 29398 ATGACCACACAGGCGAGTGG 29418
|||||

RESULT 2

ABV78222
ID ABV78222 standard; DNA; 1560 BP.

XX ABV78222;

DT 15-NOV-2002 (first entry)

XX Human MMP17 DNA SEQ ID NO 106.

XX RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;
KW virucide; protozoacide; gene; ds.

XX Homo sapiens.

XX WO200255693-A2.

XX 18-JUL-2002.

XX 09-JAN-2002; 2002WO-BP000152.

XX 09-JAN-2001; 2001DE-01000586.

PR 26-OCT-2001; 2001DE-01055280.

PR 29-NOV-2001; 2001DE-01058411.

PR 07-DEC-2001; 2001DE-01060151.

XX (RIBO-) RIBOPHARMA AG.

XX Kreutzer R, Limmer S, Rost S, Hadwiger P;

XX WPI; 2002-590671/63.

XX Inhibiting expression of target gene, useful e.g. for inhibiting

PT oncogenes, by administering double-stranded RNA complementary to the

PT target and having an overhang.

XX Claim 10; Page 176; 203pp; German.

XX The invention relates to inhibiting expression of a target gene (I) in a

CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded

CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA is complementary to (I) and at least one end of dsRNA1
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention

XX Sequence 1560 BP; 275 A; 549 C; 479 G; 257 T; 0 U; 0 Other;

Query Match 84.8%; Score 17.8; DB 6; Length 1560;

Best Local Similarity 90.5%; Pred. No. 87;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCGAGTGG 21
|||||

DB 1112 ATGACCACACAGGCGAGTGG 1132
|||||

RESULT 3

ABZ35798

ID ABZ35798 standard; DNA; 1560 BP.

XX ABZ35798;

XX 07-FEB-2003 (first entry)

XX Human MMP17 polynucleotide SEQ ID NO 106.

XX Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
KW protozoacide; gene expression; antisense; tumour; infection; plasmodium;
KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
KW Hepatitis C virus; human papilloma virus; gene; ds.

XX Homo sapiens.

XX DE10100588-A1.

XX 18-JUL-2002.

XX 09-JAN-2001; 2001DE-01000588.

XX 09-JAN-2001; 2001DE-01000588.

XX (RIBO-) RIBOPHARMA AG.

XX Kreutzer R, Limmer S, Rost S, Hadwiger P;

XX WPI; 2002-683450/74.

XX Inhibiting expression of target genes, useful e.g. for treating tumors,
PT by introducing into cells two double-stranded RNAs that are complementary
PT to the target.

XX Claim 13; Page 73-74; 100pp; German.

XX The invention relates to inhibiting expression of a target gene in a cell
CC by introducing at least two oligoribonucleotides (dsRNA1 and II), both
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
CC pairs. At least part of one strand (S1, S2) of the ds structures in each
CC of dsRNA1 and II are complementary to regions in the target gene. The
CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumours
CC or infections, especially by plasmodium or viruses/viroids (pathogenic on
CC humans, animals or plants). The method provides more effective inhibition
CC of expression than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, stability (and thus effective concentration in the cell) is improved
CC and efficiency can be increased further by pretreating the cells with
CC interferon. The present sequence is that of a target DNA of the invention

```

XX SQ Sequence 1560 BP; 275 A; 549 C; 479 G; 257 T; 0 U; 0 Other;
    Query Match      84.8%; Score 17.8; DB 6; Length 1560;
    Best Local Similarity 90.5%; Pred. No. 87;
    Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21
    |||||
Db 1112 ATGACCACACAGGCACATGG 1132

RESULT 4
ABX10041
ID ABX10041 standard; DNA; 1560 BP.
XX AC ABX10041;
XX DT 23-JAN-2003 (first entry)
XX DE Human MMP17 DNA fragment SEQ ID 106.
XX KW Oligoribonucleotide; interferon; oncogene; cytokine; id; developmental;
XX KW Prion; inhibition; human; ds.
XX OS Homo sapiens.
XX PN DE10100587-C1.
XX PD 21-NOV-2002.
XX PF 09-JAN-2001; 2001DE-01000587.
XX PR 09-JAN-2001; 2001DE-01000587.
XX PA (RIBO-) RIBOPHARMA AG.
XX PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX WPI; 2002-742209/81.
XX CC The invention describes a novel method for inhibiting expression of a
    target gene by introducing into the cell that contains the target gene at
    least one oligoribonucleotide (dsRNA) that has a double-stranded
    structure of not more than 49 consecutive nucleotides (nt), where at
    least a segment of one strand of the ds structure is complementary with
    the target gene and the cells are treated with interferon before
    introduction of dsRNA. The method is used to inhibit expression of
    target genes, particularly oncogenes, cytokine genes, id (not defined)
    protein genes; developmental or prion genes, or genes expressed in
    pathogenic organisms (particularly plasmodia) or in viruses or viroids
    (pathogenic in humans, animals or plants). Treating the cells with
    interferon greatly increases the extent to which dsRNA can inhibit
    expression of the target genes, and the effect is even greater when dsRNA
    are modified to increase their stability. ABX0936-ABX10075 represent
    gene fragments used to illustrate the method of the invention
XX SQ Sequence 1560 BP; 275 A; 549 C; 479 G; 257 T; 0 U; 0 Other;
    Query Match      84.8%; Score 17.8; DB 6; Length 1560;
    Best Local Similarity 90.5%; Pred. No. 87;
    Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21
    |||||
Db 1112 ATGACCACACAGGCACATGG 1132

RESULT 5
ABL91763
ID ABL91763 standard; DNA; 1560 BP.
XX AC ABL91763;
XX DT 28-MAY-2002 (first entry)
XX DE Human polynucleotide SEQ ID NO 106.
XX KW Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
XX KW Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
XX KW cytostatic; virucide; protozoacide; antibacterial; ds.
XX OS Homo sapiens.
XX PN DE10100586-C1.
XX PD 11-APR-2002.
XX PF 09-JAN-2001; 2001DE-01000586.
XX PR 09-JAN-2001; 2001DE-01000586.
XX PA (RIBO-) RIBOPHARMA AG.
XX PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX WPI; 2002-270454/32.
XX CC Inhibiting gene expression in cells, useful for e.g. treating tumors, by
    introducing double-stranded complementary oligonucleotide having unpaired
    terminal bases.
XX PS Claim 13; Page 78; 104pp; German.
XX CC The invention relates to a method for inhibiting expression of a target
    gene (ABL91658-ABL91797) in a cell by introducing at least one
    oligoribonucleotide that has a double-stranded structure consisting of at
    most 49 sequential nucleotide pairs, with at least part of one strand
    complementary with the target gene and has at least one end a single-
    stranded segment of 1-4 nt. The method provides oligoribonucleotides for
    antisense inhibition of gene expression useful e.g. for treating tumours
    but the oligoribonucleotides may also be directed against genes present
    in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans,
    animals or plants) or against cytokine, id, developmental or prion genes.
    The method provides more effective inhibition of gene expression than use
    of known oligonucleotides, probably because the unpaired overhang
    increases stability and thus intracellular concentration
XX SQ Sequence 1560 BP; 275 A; 549 C; 479 G; 257 T; 0 U; 0 Other;
    Query Match      84.8%; Score 17.8; DB 6; Length 1560;
    Best Local Similarity 90.5%; Pred. No. 87;
    Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21
    |||||
Db 1112 ATGACCACACAGGCACATGG 1132

RESULT 6
ABV78191
ID ABV78191 standard; DNA; 1818 BP.
XX AC ABV78191;
XX DT 15-NOV-2002 (first entry)
XX DE Human MT4MMP DNA SEQ ID NO 75.
XX KW RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;

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KW virucide; protozoacide; gene; ds.
XX
OS Homo sapiens.
XX
FN WO200255693-A2.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2002; 2002WO-EP000152.
XX
PR 09-JAN-2001; 2001DE-01000586.
PR 26-OCT-2001; 2001DE-01055280.
PR 29-NOV-2001; 2001DE-01058411.
PR 07-DEC-2001; 2001DE-01060151.
XX
FA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-590671/63.
XX
PT Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX
PS Claim 10; Page 153-154; 203pp; German.
XX
CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA is complementary to (I) and at least one end of dsRNA
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in Plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention
XX
SQ Sequence 1818 BP; 310 A; 649 C; 571 G; 288 T; 0 U; 0 Other;

Query Match      84.8%; Score 17.8; DB 6; Length 1818;
Best Local Similarity 90.5%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21
   ||||| ||||| ||||| |||||
DB 1370 ATGACCACAGGCAGATGG 1390

RESULT 7
ABZ35767
ID ABZ35767 standard; DNA; 1818 BP.
XX
AC ABZ35767;
XX
DT 07-FEB-2003 (first entry)
XX
DE Human MT4MMP polynucleotide SEQ ID NO 75.
XX
KW Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
KW protozoacide; gene expression; antisense; tumour; infection; Plasmodium;
KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
KW Hepatitis C virus; human papilloma virus; gene; ds.
XX
OS Homo sapiens.
XX
FN DE10100588-A1.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2001; 2001DE-01000588.

virucide; protozoacide; gene; ds.
XX
OS Homo sapiens.
XX
FN WO200255693-A2.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2002; 2002WO-EP000152.
XX
PR 09-JAN-2001; 2001DE-01000586.
PR 26-OCT-2001; 2001DE-01055280.
PR 29-NOV-2001; 2001DE-01058411.
PR 07-DEC-2001; 2001DE-01060151.
XX
FA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-590671/63.
XX
PT Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX
PS Claim 10; Page 153-154; 203pp; German.
XX
CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA is complementary to (I) and at least one end of dsRNA
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in Plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention
XX
SQ Sequence 1818 BP; 310 A; 649 C; 571 G; 288 T; 0 U; 0 Other;

Query Match      84.8%; Score 17.8; DB 6; Length 1818;
Best Local Similarity 90.5%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21
   ||||| ||||| ||||| |||||
DB 1370 ATGACCACAGGCAGATGG 1390

RESULT 8
ABX10010
ID ABX10010 standard; DNA; 1818 BP.
XX
AC ABX10010;
XX
DT 23-JAN-2003 (first entry)
XX
DE Human MT4MMP DNA fragment SEQ ID 75.
XX
KW Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;
KW prion; inhibition; human; ds.
XX
OS Homo sapiens.
XX
FN DE10100587-C1.
XX
PD 21-NOV-2002.
XX
PF 09-JAN-2001; 2001DE-01000587.
XX
PR 09-JAN-2001; 2001DE-01000587.
XX
FA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-742209/81.
XX
PT Inhibiting expression of target genes, e.g. oncogenes, in cells, by
PT introduction of complementary double-stranded oligoribonucleotide, after
PT treating the cell with interferon.

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XX Disclosure; Page 55; 98pp; German.

XX This invention describes a novel method for inhibiting expression of a

CC target gene by introducing into the cell that contains the target gene at

CC least one oligoribonucleotide (dsRNAi) that has a double-stranded (ds)

CC structure of not more than 49 consecutive nucleotides (nt), where at

CC least a segment of one strand of the ds structure is complementary with

CC the target gene and the cells are treated with interferon before

CC introduction of dsRNAi. The method is used to inhibit expression of

CC target genes, particularly oncogenes, cytokine genes, Id (not defined)

CC pathogen genes; developmental or prion genes, or genes expressed in

CC pathogenic organisms (particularly plasmidia) or in viruses or viroids

CC (pathogenic in humans, animals or plants). Treating the cells with

CC interferon greatly increases the extent to which dsRNA can inhibit

CC expression of the target genes, and the effect is even greater when dsRNA

CC are modified to increase their stability. ABX0936-ABX10075 represent

CC gene fragments used to illustrate the method of the invention

XX

XX Sequence 1818 BP; 310 A; 649 C; 571 G; 288 T; 0 U; 0 Other;

Query Match 84.8%; Score 17.8; DB 6; Length 1818;

Best Local Similarity 90.5%; Pred. No. 89;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCGACATGG 21

|||||

Db 1370 ATGACCACACAGGCGACATGG 1390

RESULT 9

ABL91732

ID ABL91732 standard; DNA; 1818 BP.

XX ABL91732;

XX

XX 28-MAY-2002 (first entry)

XX

XX Human polynucleotide SEQ ID NO 75.

XX

XX Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;

XX Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;

XX cytosatic; virucide; protozoacide; antibacterial; ds.

XX

XX Homo sapiens.

XX DE10100586-C1.

XX

XX 11-APR-2002.

XX

XX 09-JAN-2001; 2001DE-01000586.

XX

XX 09-JAN-2001; 2001DE-01000586.

XX

XX (RIBO-) RIBOPHARMA AG.

XX

XX Kreutzer R, Limmer S, Rost S, Hadwiger P;

XX WPI; 2002-270454/32.

XX

XX Inhibiting gene expression in cells, useful for e.g. treating tumors, by

XX introducing double-stranded complementary oligorNA having unpaired

XX terminal bases.

XX

XX Claim 13; Page 53-54; 104pp; German.

XX

XX The invention relates to a method for inhibiting expression of a target

CC gene (ABL91658-ABL91797) in a cell by introducing at least one

CC oligoribonucleotide that has a double-stranded structure consisting of at

CC most 49 sequential nucleotide pairs, with at least part of one strand

CC complementary with the target gene, and has at least one end a single-

CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for

CC antisense inhibition of gene expression useful e.g. for treating tumours

CC but the oligoribonucleotides may also be directed against genes present

CC in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans,

CC animals or plants) or against cytokine, Id, developmental or prion genes.

CC The method provides more effective inhibition of gene expression than use

CC of known oligonucleotides, probably because the unpaired overhang

CC increases stability and thus intracellular concentration

XX

XX Sequence 1818 BP; 310 A; 649 C; 571 G; 288 T; 0 U; 0 Other;

Query Match 84.8%; Score 17.8; DB 6; Length 1818;

Best Local Similarity 90.5%; Pred. No. 89;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCGACATGG 21

|||||

Db 1370 ATGACCACACAGGCGACATGG 1390

RESULT 10

AAA13389

ID AAA13389 standard; DNA; 2295 BP.

XX

XX AAA13389;

XX

XX 28-JUL-2000 (first entry)

XX

XX Human MT4-MMP matrixmetalloprotease nucleotide sequence.

XX

XX Matrix metalloprotease; MT4-MMP; treatment; arthrosis deformans;

XX Chronic rheumatoid arthritis; asthma; autoimmune disease; hepatitis;

XX atrophic dermatitis; psoriasis; contact dermatitis; hair loss; nephritis;

XX ischaemic disease; pancreatitis; arteriosclerosis; leukaemia; tumour;

XX wound; corneal ulcer; tissue damage; inflammation; cerebral apoplexia;

XX Alzheimer's disease; dementia; multiple sclerosis; Parkinson's disease;

XX gene therapy; ds.

XX

XX Homo sapiens.

XX

XX WO200018900-A1.

XX

XX 06-APR-2000.

XX

XX 29-SEP-1999; 99WO-JP005349.

XX

XX 29-SEP-1998; 98JP-00276258.

XX

XX 29-SEP-1998; 98JP-00291505.

XX

XX (SEIKI/) SEIKI M.

XX

XX Seiki M;

XX

XX WPI; 2000-293141/25.

XX

XX Physiologically-active transmembrane matrix metalloprotease polypeptide,

XX useful in screening inhibitors and activators for treating e.g. arthrosis

XX deformans, asthma and cancers.

XX

XX Example 1; Page 99-102; 113pp; Japanese.

XX

XX This sequence represents the human matrix metalloprotease (MT4-MMP 2)

CC nucleotide sequence. The invention relates to a mammalian transmembrane

CC MMP polypeptide, its variants and the DNA sequences encoding them. Also

CC included in the invention is a vector comprising the MMP DNA molecules,

CC and cells transformed using the vector. The protein, DNA and antibodies

CC directed against the polypeptide are useful in screening inhibitors and

CC activators for use in treating arthrosis deformans, chronic rheumatoid

CC arthritis, asthma, autoimmune diseases, atrophic dermatitis, psoriasis,

CC contact dermatitis, hair loss, ischaemic diseases, immune reaction

CC accompanying organ transplant, hepatitis, nephritis, pancreatitis,

CC arteriosclerosis, leukaemia, malignant tumours, wounds, corneal ulcers,

CC tissue damage or inflammation accompanying leukocytic infiltration,

CC together with brain disorders during cerebral apoplexia, Alzheimer's

CC disease, dementia, multiple sclerosis, Parkinson's disease or brain

CC tumours. The DNA can also be incorporated into a suitable vector for use
 CC in gene therapy

XX SQ Sequence 2295 BP; 401 A; 807 C; 729 G; 358 T; 0 U; 0 Other;
 Query Match 84.8%; Score 17.8; DB 3; Length 2295;
 Best Local Similarity 90.5%; Pred. No. 92;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ATGACCACACAGGCAGATGG 21
 |||||
 Db 1341 ATGACCACACAGGCACATGG 1361

RESULT 11
 AAA14351
 ID AAA14351 standard; DNA; 2295 BP.

XX AC AAA14351;

XX DT 15-AUG-2000 (first entry)

XX DE Human MT4-MMP(2) gene fragment, used as a probe.

XX KW Matrix metalloprotease; MT4-MMP(2); transmembrane; human; antibody;
 KW drug screening; diagnosis; arthritis deformans; rheumatoid arthritis;
 KW asthma; autoimmune disease; atopic dermatitis; skin disorder;
 KW ischaemic disorder; arteriosclerosis; cancer; tissue damage;
 KW inflammatory disorder; neurological disorder; probe; ss.

XX OS Homo sapiens.

XX PN WO200018805-A1.

XX PD 06-APR-2000.

XX PF 29-SEP-1999; 99WO-JP005350.

XX PR 29-SEP-1998; 98JP-00291501.

XX PR 29-SEP-1998; 98JP-00291503.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Hanai N, Furiya A;

XX DR WPI; 2000-293115/25.

XX PT Antibody immunospecific for transmembrane matrix metalloprotease
 PT polypeptide, useful in screening of inhibitors and activators as drugs
 PT for, and for diagnosis of e.g. arthritis deformans and asthma.

XX PS Example 1; Page 134-137; 152pp; Japanese.

XX CC The invention relates to antibodies against the novel murine and human
 CC transmembrane matrix metalloproteases MT4-MMP(2) (AA950502 and AA950503)
 CC and MT5-MMP (AA950504 and AA950505). The antibodies are useful for the
 CC diagnosis and screening of inhibitors and activators useful for treating
 CC or preventing a wide variety of medical conditions, such as arthritis
 CC deformans, rheumatoid arthritis, asthma, autoimmune diseases and atopic
 CC dermatitis. The anti-MT5-MMP antibodies may additionally be used to
 CC diagnose and screen therapeutic or prophylactic agents for conditions
 CC affecting the brain, such as cerebral stroke and Alzheimer's disease. The
 CC antibodies of the invention may also be used for the prevention,
 CC diagnosis and treatment of psoriasis, contact dermatitis, hair loss,
 CC ischaemic diseases, immune reaction accompanying organ transplant,
 CC hepatitis, nephritis, pancreatitis, arteriosclerosis, leukaemia,
 CC malignant tumours, wounds, corneal ulcers, tissue damage or inflammation
 CC accompanying leukocytic infiltration, dementia, multiple sclerosis,
 CC Parkinson's disease or brain tumour. The present sequence represents a
 CC fragment of the human MT4-MMP(2) gene used as a probe in an
 CC exemplification of the invention to screen a murine cDNA library for a
 CC murine MT4-MMP(2) cDNA clone

SQ Sequence 2295 BP; 401 A; 807 C; 729 G; 358 T; 0 U; 0 Other;
 Query Match 84.8%; Score 17.8; DB 3; Length 2295;
 Best Local Similarity 90.5%; Pred. No. 92;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ATGACCACACAGGCAGATGG 21
 |||||
 Db 1341 ATGACCACACAGGCACATGG 1361

RESULT 12
 AAH28234
 ID AAH28234 standard; cDNA; 2306 BP.

XX AC AAH28234;

XX DT 05-SEP-2001 (first entry)

XX DE Nucleotide sequence of matrix metalloproteinase-17.

XX KW Growth factor; protein inhibitor; protease; damaged tissue;
 KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
 KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
 KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
 KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
 KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
 KW vascular endothelial growth factor; urokinase plasminogen activator;
 KW dermal ulcer; wound; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT CDS 233..1792
 FT /*tag= a
 FT /product= "MMP-17"

XX PN WO2000149309-A2.

XX PD 12-JUL-2001.

XX PF 21-DEC-2000; 2000WO-IB001935.

XX PR 29-DEC-1999; 99GB-00030768.

XX PA (PFIZ) PFIZER LTD.

XX PA (PFIZ) PFIZER INC.

XX PI Davies MJ, Huggins JP, McIntosh FS, Occleston NL;

XX DR WPI; 2001-418351/44.

XX DR P-PSDB; AAB84619.

XX CC Composition for the treatment of damaged tissue i.e. chronic wounds and
 CC dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
 CC factor.

XX PS Disclosure; Page 567; 572pp; English.

XX CC The specification describes a pharmaceutical composition, comprising a
 CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
 CC inhibits the action of at least one specific adverse protein, i.e. a
 CC protease, that is upregulated in a damaged tissue such as a wound
 CC environment. Growth factors which are included in the composition of the
 CC invention are platelet-derived growth factor (PDGF), fibroblast growth
 CC factor (FGF), connective tissue derived growth factor (CTGF),
 CC keratinocyte-derived growth factor (KGF), transforming growth factor-beta
 CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
 CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
 CC and chrysalin. Inhibitors which are included in the composition of the
 CC invention include inhibitors of urokinase-type plasminogen activator
 CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for
 CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.

CC The present sequence encodes a human MMP-17, and is used to produce the
CC composition of the invention

SQ Sequence 2306 BP; 402 A; 810 C; 735 G; 359 T; 0 U; 0 Other;
Query Match 84.8%; Score 17.8; DB 4; Length 2306;
Best Local Similarity 90.5%; Pred. No. 92;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21

Db 1344 ATGACCACACAGGCAGATGG 1364

RESULT 13

ID ADE84832

AC ADE84832 standard; DNA; 2306 BP.

XX ADE84832;

XX 29-JAN-2004 (first entry)

XX Farnesyl transferase inhibitor modulated leukemia associated gene #51.

XX ss; cytostatic; farnesyl transferase inhibitor; gene expression;

XX quinolinone; leukemia; cancer.

XX Homo sapiens.

XX WO2003038129-A2.

XX 08-MAY-2003.

XX 30-OCT-2002; 2002WO-US034784.

XX 30-OCT-2001; 2001US-0338997P.

XX 30-OCT-2001; 2001US-0340081P.

XX 30-OCT-2001; 2001US-0340938P.

XX 30-OCT-2001; 2001US-0341012P.

XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

XX Raponi M;

XX WPI; 2003-513497/48.

XX Determining whether a patient will respond to treatment with a farnesyl
PT transferase inhibitor, by analyzing the expression of gene that is
PT differentially modulated in the presence of the inhibitor.

XX Disclosure; SEQ ID NO 51; 346pp; English.

XX The invention relates to a method of determining whether a patient will
CC respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC analyzing the expression of gene that is differentially modulated in the
CC presence of an FTI. The method is useful for determining whether a
CC patient will respond to treatment with a FTI such as (B)-6- (amino(4-
CC chlorophenyl) (1-methyl-1H-imidazol-5-yl)methyl)-4- (3-chlorophenyl)-1-
CC methyl-2- (1H) quinolinone, monitoring the therapy of a patient, treating a
CC patient with leukemia with FTI if the analysis indicates that the patient
CC will respond. This sequence corresponds to a gene whose expression may be
CC modulated in the presence of FTI.

XX Sequence 2306 BP; 402 A; 810 C; 735 G; 359 T; 0 U; 0 Other;

Query Match 84.8%; Score 17.8; DB 10; Length 2306;

Best Local Similarity 90.5%; Pred. No. 92;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21

Db 1344 ATGACCACACAGGCAGATGG 1364

RESULT 14

AAA14340

XX AAA14340 standard; cDNA; 2423 BP.

XX AAA14340;

XX 15-AUG-2000 (first entry)

XX cDNA encoding human transmembrane matrix metalloprotease MT4-MMP(2).

XX Matrix metalloprotease; MT4-MMP(2); transmembrane; human; antibody;
KW drug screening; diagnosis; arthritis deformans; rheumatoid arthritis;
KW asthma; autoimmune disease; atopic dermatitis; skin disorder;
KW ischaemic disorder; arteriosclerosis; cancer; tissue damage;
KW inflammatory disorder; neurological disorder; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 100..1917

XX /tag= a

XX /product= "Human transmembrane matrix metalloprotease MT4-MMP(2)"

XX WO200018805-A1.

XX 06-APR-2000.

XX 29-SEP-1999; 99WO-JP005350.

XX 29-SEP-1998; 98JP-00291501.

XX 29-SEP-1998; 98JP-00291503.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Hanai N, Furuya A;

XX WPI; 2000-293115/25.

XX P-PSDB; AAY90503.

XX Antibody immunospecific for transmembrane matrix metalloprotease
PT polypeptide, useful in screening of inhibitors and activators as drugs
PT for, and for diagnosis of e.g. arthritis deformans and asthma.

XX Example 2; Page 102-108; 152pp; Japanese.

XX This sequence represents cDNA encoding a novel human transmembrane matrix
CC metalloprotease MT4-MMP(2). MT4-MMP(2) has physiological activity
CC different to that of MT4-MMP. The invention relates to antibodies against
CC both murine and human MT4-MMP(2) (AAY90502 and AAY90503) and to
CC antibodies against a novel murine and human transmembrane matrix

CC metalloprotease MT5-MMP (AAY90504 and AAY90505). The antibodies are
CC useful for the diagnosis and screening of inhibitors and activators
CC useful for treating or preventing a wide variety of medical conditions,
CC such as arthritis deformans, rheumatoid arthritis, asthma, autoimmune
CC diseases and atopic dermatitis. The anti-MT5-MMP antibodies may
CC additionally be used to diagnose and screen therapeutic or prophylactic
CC agents for conditions affecting the brain, such as cerebral stroke and
CC Alzheimer's disease. The antibodies of the invention may also be used for
CC the prevention, diagnosis and treatment of psoriasis, contact dermatitis,
CC hair loss, ischaemic diseases, immune reaction accompanying organ
CC transplant, hepatitis, nephritis, pancreatitis, arteriosclerosis,
CC leukaemia, malignant tumours, wounds, corneal ulcers, tissue damage or
CC inflammation accompanying leukocytic infiltration, dementia, multiple
CC sclerosis, Parkinson's disease or brain tumour

XX Sequence 2423 BP; 404 A; 871 C; 794 G; 354 T; 0 U; 0 Other;

Query Match 84.8%; Score 17.8; DB 3; Length 2423;

Best Local Similarity 90.5%; Pred. No. 93;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ATGACCACACAGGCGAGTGG 21
DB 1469 ATGACCACACAGGCGAGTGG 1489

RESULT 15

ABZ20920
ID ABZ20920 standard; cDNA; 2423 BP.
XX
XX AC ABZ20920;
XX
XX DT 26-MAR-2003 (first entry)
XX
XX DE MT4-MMP catalytic domain antibody related coding sequence.
XX
XX KW MT4-MMP; catalytic domain; antibody; inflammation; cancer; gene;
KW membrane type-matrix metalloproteinase; antiinflammatory; antirheumatoid;
KW antiarthritic; rheumatoid arthritis; cytostatic; human; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2002101046-A1.
XX
XX PD 19-DEC-2002.
XX
XX PF 11-JUN-2002; 2002WO-JP005788.
XX
XX PR 11-JUN-2001; 2001JP-00176256.
XX
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX PI Miki I, Ohta S, Shitara K, Furuya A;
XX
XX DR WPI; 2003-148808/14.
XX
XX DR P-PSDB; AAO19713.
XX
XX PT Monoclonal antibody specifically binding to natural or solubilized MT4-MMP, applicable in diagnosis and remedies for MT4-MMP participated diseases e.g. inflammations and cancer particularly rheumatoid arthritis.
XX
XX PS Example 1; Page 50-54; 63pp; Japanese.
XX
XX CC The present invention relates to a monoclonal antibody which binds specifically to the MT4-MMP (membrane type-matrix metalloproteinase) catalytic domain. The antibody is applicable in diagnosis and remedies for MT4-MMP participated diseases e.g. inflammations and cancer particularly rheumatoid arthritis. The present sequence is a human coding sequence shown in the exemplification of the invention
XX
XX SQ Sequence 2423 BP; 404 A; 871 C; 794 G; 354 T; 0 U; 0 Other;

Query Match 84.8%; Score 17.8; DB 8; Length 2423;
Best Local Similarity 90.5%; Pred. No. 93;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ATGACCACACAGGCGAGTGG 21
DB 1469 ATGACCACACAGGCGAGTGG 1489

Search completed: May 15, 2005, 11:25:18
Job time : 17.1953 secs

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OM nucleic - nucleic search, using sw model

Run on: May 15, 2005, 11:11:51 ; Search time 4.6102 Seconds
(without alignments)
7453.434 Million cell updates/sec

Title: US-10-764-075-2

Perfect score: 21

Sequence: 1 atgaccacacagggcagatgg 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgn2_6/prodata/1/ina/5A COMB.seq.*

2: /cgn2_6/prodata/1/ina/5B COMB.seq.*

3: /cgn2_6/prodata/1/ina/6A COMB.seq.*

4: /cgn2_6/prodata/1/ina/6B COMB.seq.*

5: /cgn2_6/prodata/1/ina/PCITUS COMB.seq.*

6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.8	80.0	224	4	US-09-313-294A-7452
2	16.8	80.0	2354	3	US-09-810-671-1
3	16.8	80.0	2354	4	US-10-109-854-1
4	16.8	80.0	2354	4	US-10-339-656-1
5	16.8	80.0	2446	2	US-09-016-000-9
6	16.8	80.0	9769	3	US-08-961-527-30
7	16.8	80.0	21234	3	US-09-810-671-3
8	16.8	80.0	21234	4	US-10-109-854-3
9	16.8	80.0	21234	4	US-10-339-656-3
10	16.8	80.0	100836	4	US-09-949-016-12871
11	16.8	80.0	100837	4	US-09-949-016-17063
12	16.8	80.0	149543	4	US-09-949-016-15947
13	16.8	80.0	248968	4	US-09-949-016-12614
14	16.8	80.0	250958	4	US-09-949-016-16061
15	16.2	77.1	601	4	US-09-949-016-169568
16	16.2	77.1	884	4	US-09-790-045-11
17	16.2	77.1	884	4	US-10-222-577-11
18	16.2	77.1	884	4	US-10-222-578-11
19	16.2	77.1	1200	4	US-09-598-401C-36
20	16.2	77.1	17000	4	US-09-679-2999A-18
21	16.2	77.1	26103	4	US-09-949-016-16841
22	16.2	77.1	160759	4	US-09-949-016-16514
23	16.2	77.1	235064	4	US-09-949-016-15390
24	16.2	77.1	421491	4	US-09-949-016-12805
25	16.2	77.1	421491	4	US-09-949-016-12060
26	15.8	75.2	471	4	US-09-513-999C-992
27	15.8	75.2	537	4	US-09-513-999C-993

C 28	15.8	75.2	601	4	US-09-949-016-91184	Sequence 91184, A
C 29	15.8	75.2	601	4	US-09-949-016-201853	Sequence 201853, A
C 30	15.8	75.2	1174	2	US-08-481-658B-39	Sequence 39, Appl
C 31	15.8	75.2	1174	2	US-08-477-504A-39	Sequence 39, Appl
C 32	15.8	75.2	1174	2	US-08-486-756A-39	Sequence 39, Appl
C 33	15.8	75.2	1174	2	US-08-485-862B-39	Sequence 39, Appl
C 34	15.8	75.2	1174	3	US-08-487-077A-39	Sequence 39, Appl
C 35	15.8	75.2	1174	3	US-08-485-863A-39	Sequence 39, Appl
C 36	15.8	75.2	1174	3	US-08-485-049D-39	Sequence 39, Appl
C 37	15.8	75.2	1174	3	US-09-178-115-39	Sequence 39, Appl
C 38	15.8	75.2	1174	3	US-09-177-776-39	Sequence 39, Appl
C 39	15.8	75.2	1174	4	US-09-772-719B-39	Sequence 39, Appl
C 40	15.8	75.2	1505	4	US-09-620-312D-544	Sequence 544, App
C 41	15.8	75.2	4079	4	US-09-016-434-1173	Sequence 1173, App
C 42	15.8	75.2	4425	4	US-09-949-016-5564	Sequence 5564, Ap
C 43	15.8	75.2	4426	3	US-09-658-687A-3	Sequence 3, Appli
C 44	15.8	75.2	4426	4	US-09-949-016-843	Sequence 843, App
C 45	15.8	75.2	4426	4		

ALIGNMENTS

RESULT 1
US-09-313-294A-7452/c
; Sequence 7452, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 7452
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700381752H1
US-09-313-294A-7452

Query Match 80.0%; Score 16.8; DB 4; Length 224;
Best Local Similarity 90.0%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGACACACACAGGCAGATGG 21
DB 39 TGTCCACACAGGCTGATGG 20

RESULT 2
US-09-810-671-1
; Sequence 1, Application US/09810671
; Patent No. 6455291
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000758
; CURRENT APPLICATION NUMBER: US/09/810,671
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2354
; TYPE: DNA
; ORGANISM: Human

US-09-810-671-1

Query Match 80.0%; Score 16.8; DB 3; Length 2354;
Best Local Similarity 90.0%; Pred. No. 1e+02; Mismatches 0; Gaps 0;
Matches 18; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 2 TGACCACACAGGCAGATGG 21
|||||
DB 704 TGACCACATCAGGCAGATGG 723

RESULT 3

US-10-109-854-1
; Sequence 1, Application US/10109854
; Patent No. 6630337
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000758DIV
; CURRENT APPLICATION NUMBER: US/10/109,854
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/227,470
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/810,671
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2354
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-109-854-1

Query Match 80.0%; Score 16.8; DB 4; Length 2354;
Best Local Similarity 90.0%; Pred. No. 1e+02; Mismatches 0; Gaps 0;
Matches 18; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 2 TGACCACACAGGCAGATGG 21
|||||
DB 704 TGACCACATCAGGCAGATGG 723

RESULT 4

US-10-339-656-1
; Sequence 1, Application US/10339656
; Patent No. 6733978
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000758DIV2
; CURRENT APPLICATION NUMBER: US/10/339,656
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 10/109,854
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/810,671
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/227,470
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2354
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-339-656-1

Query Match 80.0%; Score 16.8; DB 4; Length 2354;
Best Local Similarity 90.0%; Pred. No. 1e+02; Mismatches 0; Gaps 0;
Matches 18; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 2 TGACCACACAGGCAGATGG 21
|||||
DB 704 TGACCACATCAGGCAGATGG 723

RESULT 5

US-09-016-000-9
; Sequence 9, Application US/09016000
; Patent No. 5962232
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; TITLE OF INVENTION: PROTEIN KINASE MOLECULES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Inocyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,000
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0465 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2446 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: NEUTFMT01
; CLONE: 339963
US-09-016-000-9

Query Match 80.0%; Score 16.8; DB 2; Length 2446;
Best Local Similarity 90.0%; Pred. No. 1e+02; Mismatches 0; Gaps 0;
Matches 18; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 2 TGACCACACAGGCAGATGG 21
|||||
DB 817 TGACCACATCAGGCAGATGG 836

RESULT 6

US-08-961-527-30/c
; Sequence 30, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch

;; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 391
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/961,527
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brookes, A. Anders
;; REGISTRATION NUMBER: 36,373
;; REFERENCE/DOCKET NUMBER: PB340P1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 30:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9769 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
US-08-961-527-30

Query Match 80.0%; Score 16.8; DB 3; Length 9769;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACCACACAGGCAGATGG 21
DB 3808 TGACCAACACAGGCAGTGG 3789

RESULT 7
US-09-810-671-3
; Sequence 3, Application US/09810671
; Patent No. 6455291
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/09/810,671
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 21234
; TYPE: DNA
; ORGANISM: Human
US-09-810-671-3

Query Match 80.0%; Score 16.8; DB 3; Length 21234;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACCACACAGGCAGATGG 21
DB 8379 TGACCACATCAGGCAGATGG 8398

RESULT 8
US-10-109-854-3
; Sequence 3, Application US/10109854
; Patent No. 6630397
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/10/109,854
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/227,470
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/810,671
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 21234
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-109-854-3

Query Match 80.0%; Score 16.8; DB 4; Length 21234;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACCACACAGGCAGATGG 21
DB 8379 TGACCACATCAGGCAGATGG 8398

RESULT 9
US-10-339-656-3
; Sequence 3, Application US/10339656
; Patent No. 6733978
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/10/339,656
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 10/109,854
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/810,671
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/227,470
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 21234
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-339-656-3

Query Match 80.0%; Score 16.8; DB 4; Length 21234;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACCACACAGGCAGATGG 21
DB 8379 TGACCACATCAGGCAGATGG 8398

RESULT 10
US-09-949-016-12871/c
; Sequence 12871, Application US/09949016
; Patent No. 6812339

US-09-949-016-17063/c
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12871
; LENGTH: 100836
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(100836)
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12871
Query Match 80.0%; Score 16.8; DB 4; Length 100836;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGACCACACAAAGGCAGATGG 21
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DB 68341 TGACCACACAAAGGTGTGATGG 68322

RESULT 11
US-09-949-016-17063/c
; Sequence 17063, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17063
; LENGTH: 100837
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(100837)
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-17063
Query Match 80.0%; Score 16.8; DB 4; Length 100837;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGACCACACAAAGGCAGATGG 21
|||||
DB 68341 TGACCACACAAAGGTGTGATGG 68322

RESULT 12

US-09-949-016-15947/c
; Sequence 15947, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15947
; LENGTH: 149543
; TYPE: DNA
; ORGANISM: Human
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12614/c
Query Match 80.0%; Score 16.8; DB 4; Length 149543;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGACCACACAAAGGCAGATGG 21
|||||
DB 52555 TGACCACACAAAGGTGTGATGG 52536

RESULT 13
US-09-949-016-12614/c
; Sequence 12614, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12614
; LENGTH: 248968
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(248968)
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12614
Query Match 80.0%; Score 16.8; DB 4; Length 248968;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGACCACACAAAGGCAGATG 20
|||||
DB 67410 ATGAAACACAAAGGCAGATG 67391

RESULT 14
US-09-949-016-16061/c

; Sequence 16061, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16061
; LENGTH: 250958
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(250958)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16061

Query Match 80.0%; Score 16.8; DB 4; Length 250958;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATG 20
||| |||||
DB 117400 ATGAAAACACAGGCAGATG 117381

RESULT 15
US-09-949-016-169568/c
; Sequence 169568, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 169568
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-169568

Query Match 77.1%; Score 16.2; DB 4; Length 601;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21
||| |||||
DB 455 ATGAACACACAGGCAGATGG 435

Search completed: May 15, 2005, 14:23:03
Job time : 8.6102 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2005, 12:53:36 ; Search time 15.5004 Seconds
(without alignments)
8291.679 Million cell updates/sec

Title: US-10-764-075-2

Perfect score: 21
Sequence: 1 atgaccacacaggcagatgg 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5662332 seqs, 3060109652 residues

Total number of hits satisfying chosen parameters: 11324664

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	18	US-10-764-075-2
2	21	100.0	1136	18	US-10-764-075-1
3	21	100.0	1820	19	US-10-699-936-16
4	21	100.0	2304	19	US-10-699-936-7
5	21	100.0	2304	19	US-10-699-936-11
6	21	100.0	24774	19	US-10-889-447-3
7	21	100.0	28920	19	US-10-889-447-5
8	21	100.0	28920	19	US-10-889-447-6
9	21	100.0	29291	19	US-10-889-447-4
10	21	100.0	29430	19	US-10-889-447-7
11	21	100.0	29727	18	US-10-839-729-15
12	21	100.0	29727	18	US-10-827-757-1
13	21	100.0	29727	19	US-10-889-447-8
14	21	100.0	29727	19	US-10-699-936-1
15	21	100.0	29736	18	US-10-839-729-17
16	21	100.0	29736	19	US-10-889-447-9
17	21	100.0	29736	19	US-10-699-936-3
18	21	100.0	29742	18	US-10-839-729-16
19	21	100.0	29742	19	US-10-808-187-15
20	21	100.0	29742	19	US-10-808-187-16
21	21	100.0	29742	19	US-10-808-187-240
22	21	100.0	29742	19	US-10-808-187-737
23	21	100.0	29742	19	US-10-808-187-1108
24	21	100.0	29742	19	US-10-808-187-1590
25	21	100.0	29742	19	US-10-808-187-1965
26	21	100.0	29742	19	US-10-889-447-10
27	21	100.0	29751	18	US-10-839-729-14
28	21	100.0	29751	19	US-10-856-529-1
29	21	100.0	29751	19	US-10-626-879-67
30	21	100.0	29751	19	US-10-889-447-1
31	21	100.0	29751	19	US-10-889-447-2
32	21	100.0	29751	19	US-10-699-936-2
33	17.8	84.8	553	13	US-10-027-632-305207
34	17.8	84.8	553	17	US-10-027-632-305207
35	17.8	84.8	1560	18	US-10-384-339C-106
36	17.8	84.8	1818	18	US-10-384-339C-75
37	17.8	84.8	2295	16	US-10-406-209-17
38	17.8	84.8	2306	16	US-10-131-985-50
39	17.8	84.8	2306	18	US-10-283-975A-51
40	17.8	84.8	2306	19	US-10-901-417-50
41	17.8	84.8	2412	17	US-10-425-114-26875
42	17.8	84.8	2423	16	US-10-406-209-4
43	17.8	84.8	2423	18	US-10-480-464-5
44	17.8	84.8	2438	17	US-10-191-997-131
45	17.8	84.8	2438	17	US-10-439-388-70

ALIGNMENTS

RESULT 1
US-10-764-075-2
; Sequence 2, Application US/10764075
; Publication NO. US20040265796A1
; GENERAL INFORMATION:
; APPLICANT: Briesse, Thomas
; APPLICANT: Lipkin, Ian W.
; APPLICANT: Palacios, Gustavo
; APPLICANT: Jabado, Omar
; TITLE OF INVENTION: Methods and Kits for Detecting SARS-Associated Coronavirus
; FILE REFERENCE: 5199-87
; CURRENT APPLICATION NUMBER: US/10764,075
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: Provisional Application 60/463,704
; PRIOR FILING DATE: 2003-04-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-764-075-2

Query Match 100.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21
DB 1 ATGACCACACAGGCAGATGG 21

RESULT 2
US-10-764-075-1
; Sequence 1, Application US/10764075
; Publication No. US20040265796A1
; GENERAL INFORMATION:
; APPLICANT: Briese, Thomas
; APPLICANT: Lipkin, Ian W.
; APPLICANT: Palacios, Gustavo
; APPLICANT: Jabado, Omar
; TITLE OF INVENTION: Methods and Kits for Detecting SARS-Associated Coronavirus
; FILE REFERENCE: 5199-87
; CURRENT APPLICATION NUMBER: US/10/764,075
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: Provisional Application 60/463,704
; PRIOR FILING DATE: 2003-04-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1136
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic nucleic acid sequence that includes the 3' non-coding
; OTHER INFORMATION: region of the SARS-associated coronavirus genome and a portion of
; OTHER INFORMATION: the N gene of the SARS-associated coronavirus genome
US-10-764-075-1

Query Match 100.0%; Score 21; DB 18; Length 1136;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACCACACAAAGGCAGATGG 21
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Db 893 ATGACCACACAAAGGCAGATGG 913

RESULT 3
US-10-699-936-16
; Sequence 16, Application US/10699936
; Publication No. US20050095582A1
; GENERAL INFORMATION:
; APPLICANT: Gillim-Ross, Laura
; APPLICANT: Taylor, Jill
; APPLICANT: Scholl, David R.
; APPLICANT: Wentworth, David E.
; TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
; TITLE OF INVENTION: Syndrome Coronavirus
; FILE REFERENCE: DHI-07986
; CURRENT APPLICATION NUMBER: US/10/699,936
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: SARS-CoV ZJ-HZ01
US-10-699-936-16

Query Match 100.0%; Score 21; DB 19; Length 1620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACCACACAAAGGCAGATGG 21
|||||
Db 1353 ATGACCACACAAAGGCAGATGG 1373

RESULT 4
US-10-699-936-7
; Sequence 7, Application US/10699936
; Publication No. US20050095582A1
; GENERAL INFORMATION:

; APPLICANT: Gillim-Ross, Laura
; APPLICANT: Taylor, Jill
; APPLICANT: Scholl, David R.
; APPLICANT: Wentworth, David E.
; APPLICANT: Jollick, Joseph D.
; TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
; TITLE OF INVENTION: Syndrome Coronavirus
; FILE REFERENCE: DHI-07986
; CURRENT APPLICATION NUMBER: US/10/699,936
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 2304
; TYPE: DNA
; ORGANISM: SARS-CoV Shanghai LY
US-10-699-936-7

Query Match 100.0%; Score 21; DB 19; Length 2304;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACCACACAAAGGCAGATGG 21
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Db 2033 ATGACCACACAAAGGCAGATGG 2053

RESULT 5
US-10-699-936-11
; Sequence 11, Application US/10699936
; Publication No. US20050095582A1
; GENERAL INFORMATION:
; APPLICANT: Gillim-Ross, Laura
; APPLICANT: Taylor, Jill
; APPLICANT: Scholl, David R.
; APPLICANT: Wentworth, David E.
; APPLICANT: Jollick, Joseph D.
; TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
; TITLE OF INVENTION: Syndrome Coronavirus
; FILE REFERENCE: DHI-07986
; CURRENT APPLICATION NUMBER: US/10/699,936
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 2304
; TYPE: DNA
; ORGANISM: SARS coronavirus Shanghai LY
US-10-699-936-11

Query Match 100.0%; Score 21; DB 19; Length 2304;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACCACACAAAGGCAGATGG 21
|||||
Db 2033 ATGACCACACAAAGGCAGATGG 2053

RESULT 6
US-10-889-447-3
; Sequence 3, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 24774
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate BJ01
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-3

Query Match      100.0%; Score 21; DB 19; Length 24774;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGACCACACAAAGGCAGATGG 21
      |||||||
Db      24511 ATGACCACACAAAGGCAGATGG 24531

RESULT 7
US-10-889-447-5
; Sequence 5, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 28920
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate BJ03
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-5

Query Match      100.0%; Score 21; DB 19; Length 28920;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGACCACACAAAGGCAGATGG 21
      |||||||
Db      28660 ATGACCACACAAAGGCAGATGG 28680

RESULT 8
US-10-889-447-6
; Sequence 6, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 28920
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate BJ04
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-6

Query Match      100.0%; Score 21; DB 19; Length 28920;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGACCACACAAAGGCAGATGG 21
      |||||||
Db      29029 ATGACCACACAAAGGCAGATGG 29049

RESULT 9
US-10-889-447-4
; Sequence 4, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 29291
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate BJ02
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-4

Query Match      100.0%; Score 21; DB 19; Length 29291;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGACCACACAAAGGCAGATGG 21
      |||||||
Db      29029 ATGACCACACAAAGGCAGATGG 29049

RESULT 10
US-10-889-447-7
; Sequence 7, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 29430
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate GZ01
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-7
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```
Query Match      100.0%; Score 21; DB 19; Length 29430;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGACCACACAGGCAGATGG 21
Db      29163 ATGACCACACAGGCAGATGG 29183

RESULT 11
US-10-839-729-15
; Sequence 15, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK 013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 29727
; TYPE: DNA
; ORGANISM: SARS Coronavirus
US-10-839-729-15

Query Match      100.0%; Score 21; DB 18; Length 29727;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGACCACACAGGCAGATGG 21
Db      29398 ATGACCACACAGGCAGATGG 29418

RESULT 12
US-10-827-757-1
; Sequence 1, Application US/10827757
; Publication No. US20050004071A1
; GENERAL INFORMATION:
; APPLICANT: Comper, Wayne
; TITLE OF INVENTION: Charged Polysaccharides Resistant To Lysosomal Degradation During
; TITLE OF INVENTION: Kidney Filtration And Renal Passage And Their Use To Treat Or
; TITLE OF INVENTION: Prevent Infection By Coronaviruses
; FILE REFERENCE: 11213-007-999
; CURRENT APPLICATION NUMBER: US/10/827,757
; CURRENT FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: 60/464,294
; PRIOR FILING DATE: 2003-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 29727
; TYPE: DNA
; ORGANISM: SARS-related coronavirus (Urbani strain)
US-10-827-757-1

Query Match      100.0%; Score 21; DB 18; Length 29727;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGACCACACAGGCAGATGG 21
Db      29398 ATGACCACACAGGCAGATGG 29418

RESULT 13
US-10-889-447-8
```

```
; Sequence 8, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29727
; TYPE: DNA
; ORGANISM: SARS coronavirus Urbani
US-10-889-447-8

Query Match      100.0%; Score 21; DB 19; Length 29727;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGACCACACAGGCAGATGG 21
Db      29398 ATGACCACACAGGCAGATGG 29418

RESULT 14
US-10-699-936-1
; Sequence 1, Application US/10699936
; Publication No. US20050095582A1
; GENERAL INFORMATION:
; APPLICANT: Gillim-Ross, Laura
; APPLICANT: Taylor, Jill
; APPLICANT: Scholl, David R.
; APPLICANT: Wentworth, David E.
; APPLICANT: Jollick, Joseph D.
; TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
; FILE REFERENCE: DHI-07986
; CURRENT APPLICATION NUMBER: US/10/699,936
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 29727
; TYPE: DNA
; ORGANISM: SARS coronavirus Urbani
US-10-699-936-1

Query Match      100.0%; Score 21; DB 19; Length 29727;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGACCACACAGGCAGATGG 21
Db      29398 ATGACCACACAGGCAGATGG 29418

RESULT 15
US-10-839-729-17
; Sequence 17, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK 013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
```

```
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 29736
; TYPE: DNA
; ORGANISM: SARS Coronavirus
US-10-839-729-17
```

```
Query Match      . 100.0%; Score 21; DB 18; Length 29736;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Qy      1 ATGACCACACAGGCAGATGG 21
      |||||
Db      29383 ATGACCACACAGGCAGATGG 29403
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Job time : 16.5004 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2005, 11:03:36 ; Search time 92.4581 Seconds
(without alignments)
8645.536 Million cell updates/sec

Title: US-10-764-075-2

Perfect score: 21
Sequence: 1 atgaccacacagggatgg 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18.4	87.6	592	7	CO664875
C 2	18.4	87.6	1578	2	BF032477
C 3	18	85.7	772	2	BF696011
C 4	18	85.7	1139	9	CL104513
5	17.8	84.8	295	7	CN924279
6	17.8	84.8	329	7	T77190
7	17.8	84.8	356	1	AL119881
8	17.8	84.8	456	8	AQ669320
9	17.8	84.8	482	8	AQ133467
C 10	17.8	84.8	486	8	AQ880134
C 11	17.8	84.8	506	7	R17506
C 12	17.8	84.8	536	4	B1536734
C 13	17.8	84.8	547	9	CE836567
C 14	17.8	84.8	547	7	CF804618
C 15	17.8	84.8	558	4	BJ200351
C 16	17.8	84.8	606	7	CN853628
C 17	17.8	84.8	651	9	CE295750
C 18	17.8	84.8	659	4	BM015637
C 19	17.8	84.8	689	9	CE457443
C 20	17.8	84.8	721	4	BG768359
C 21	17.8	84.8	772	2	BE281640
C 22	17.8	84.8	886	5	BQ678947
C 23	17.8	84.8	894	5	BX389435
C 24	17.8	84.8	919	5	BQ953874

25	17.8	84.8	919	5	BUI79230
26	17.8	84.8	957	2	BF347731
27	17.8	84.8	970	4	BG251251
28	17.8	84.8	982	5	BQ680344
29	17.8	84.8	1017	5	BUI67886
C 30	17.8	84.8	1125	5	BX440072
31	17.8	84.8	1157	5	BQ955716
C 32	17.8	84.8	2438	3	BC045610
C 33	17.4	82.9	410	2	BE627254
C 34	17.4	82.9	440	8	AQ221669
C 35	17.4	82.9	445	1	AI426376
C 36	17.4	82.9	445	8	AQ244968
C 37	17.4	82.9	560	4	BM822423
C 38	17.4	82.9	695	9	CE631183
C 39	17.4	82.9	705	8	CC004155
40	17.4	82.9	847	8	CC392087
41	17.4	82.9	3606	3	AK036023
42	17	81.0	371	4	BG009169
C 43	17	81.0	457	8	AQ666653
C 44	17	81.0	529	2	BE010668
C 45	17	81.0	576	2	AV975852

ALIGNMENTS

RESULT 1
CO664875/c
LOCUS CO664875 592 bp mRNA linear EST 23-JUL-2004
DEFINITION DG40-1741l2 DG40-uterus Canis familiaris cdna 3', mRNA sequence.
ACCESSION CO664875
VERSION CO664875.1 GI:50581665
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 592)
AUTHORS Schluter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
Henrich, J. and Loebbert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schluter
LION bioscience AG
Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schluter@lionbioscience.com.

FEATURES

source

Location/Qualifiers
1..592
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG40-uterus"
/note="Organ: uterus; Vector: Dog pBluescript LION"

ORIGIN

Query Match 87.6%; Score 18.4; DB 7; Length 592;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGACCACACAGGCAGATGG 21
|||||
DB 525 TGACCACACAGGCAGATGG 506
|||||

RESULT 2

BF032477/c
LOCUS BF032477 1578 bp mRNA linear EST 20-OCT-2000

DEFINITION 60145297F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856626 5',
mRNA sequence.
ACCESSION BF032477
VERSION BF032477.1 GI:10740177
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1578)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DP
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LAM9585 row: j column: 19
High quality sequence start: 23
High quality sequence stop: 182.

FEATURES

Location/Qualifiers

1..1578
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3856626"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_66"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site.1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 87.6%; Score 18.4; DB 2; Length 1578;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGACCACACAGGCAGATGG 21
||||| ||||| ||||| |||||
Db 652 ATGACCACACAGGCAGATGG 632

RESULT 3
BF696011/c
LOCUS
DEFINITION 601852008F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076017 5',
mRNA sequence.
ACCESSION BF696011
VERSION BF696011.1 GI:11981430
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 772)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>
Plate: LCM928 row: p column: 02
High quality sequence stop: 765.

FEATURES

source

1..772
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4076017"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_56"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 85.7%; Score 18; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ACCACACAGGCAGATGG 21
||||| ||||| ||||| |||||
Db 590 ACCACACAGGCAGATGG 573
RESULT 4
CL104513
LOCUS
DEFINITION CL104513 1139 bp DNA linear GSS 05-JAN-2004
ISB1-43B21.T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-43B21,
genomic survey sequence.
ACCESSION CL104513
VERSION CL104513.1 GI:40598148
KEYWORDS GSS.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 1139)
AUTHORS Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence start: 25
High quality sequence stop: 765.

FEATURES

source

1..1139
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
/clone="ISB1-43B21"
/clone_lib="ISB1"
/note="Vector: pBelobAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"

ORIGIN

Query Match 85.7%; Score 18; DB 9; Length 1139;

Best Local Similarity 100.0%; Pred. No. 9.5e+02; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGCA 18
|||||
Db 323 ATGACCACACAGGCAGCA 340

RESULT 5
CN924279
LOCUS
DEFINITION
000414AELA009380HT (AELA) Royal Gala young expanding leaf Malus x domestica cDNA clone AELA009380, mRNA sequence.
CN924279
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Malus x domestica (cultivated apple)

REFERENCE
AUTHORS
Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave, A.

TITLE
JOURNAL
COMMENT
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
Location/Qualifiers

FEATURES
Source

1..295
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AELA009380"
/tissue_type="Leaf"
/dev_stage="Young, expanding"
/clone_lib="(AELA) Royal Gala young expanding leaf"
/note="Vector: pBK-CMV; Library sequenced by Genesis Research & Development"

ORIGIN

Query Match 84.8%; Score 17.8; DB 7; Length 295;
Best Local Similarity 90.5%; Pred. No. 1e+03; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGCATGG 21
|||||
Db 49 ATGACCATAGAGGCAGATGG 69

RESULT 6
T77190
LOCUS
DEFINITION
Y95b09 r1 Soares infant brain INTB Homo sapiens cDNA clone IMAGE:23715 5' similar to SP:COG2_MOUSE F33434 72 KD TYPE IV COLLAGENASE PRECURSOR ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
T77190.1 GI:694393
EST.
Homo sapiens (human)

REFERENCE
AUTHORS
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rafkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and

TITLE
JOURNAL
COMMENT

Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 1466

High quality sequence stops: 249 Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1466 Std Error: 0.00
Seq primer: M13RP1

High quality sequence stop: 249.

FEATURES
source

Location/Qualifiers
1..329
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:396062"
/db_xref="taxon:9606"
/clone="IMAGE:23715"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain 1N1B"
/note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo (dT) primer [5' AACTGGAGATTCGGCCGAGGAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 84.8%; Score 17.8; DB 7; Length 329;
Best Local Similarity 90.5%; Pred. No. 1e+03; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21
|||||
Db 212 ATGACCACAGGCACATGG 232

RESULT 7
AL119881

LOCUS

DEFINITION
AL119881 356 bp mRNA linear EST 04-SEP-2003
DKFZp761M2224 r1 761 (synonym: hamy2) Homo sapiens cDNA clone IMAGE:23715 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AL119881.1 GI:5925780
EST.
Homo sapiens (human)

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 356)
Bloecker, H., Boecker, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Bloecker, et al.)
Unpublished (1999)
Contact: MIPS

TITLE
JOURNAL
COMMENT

MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.

No s1 sequence available.
This clone (DKFZp761M2224) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

```

1..356
Location/Qualifiers
  /organism="Homo sapiens"
  /mol_type="rRNA"
  /db_xref="taxon:9606"
  /clone="DKFZp761M2224"
  /tissue_type="amygdala"
  /dev_stage="adult"
  /lab_host="DH10B"
  /clone_lib="761 (synonym: hamy2)"
  /note="Vector: pSPori1; Site_1: NotI; Site_2: SalI"

```

ORIGIN

```

Query Match      84.8%; Score 17.8; DB 1; Length 356;
Best Local Similarity 90.5%; Pred. No. 1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGACCACACAGGCAGATGG 21

Db 210 ATGACCACACAGGCAGATGG 230

RESULT 8

A0669320

LOCUS

DEFINITION HS 5364 Al E02 T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=940 Col=3 Row=I, genomic survey sequence.

ACCESSION

A0669320

VERSION

A0669320.1

GI:5202066

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

10449764

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)

or from Research h Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 940 row: I column: 3

Seq primer: T7

Class: BAC ends

High quality sequence stop: 456.

Location/Qualifiers

1..456

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=940 Col=3 Row=I"

/sex="male"

/clone_lib="RPCI-11 Human Male BAC Library"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

ORIGIN

```

Query Match      84.8%; Score 17.8; DB 8; Length 456;
Best Local Similarity 90.5%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21
    ||||| ||||| ||||| |||||
Db 357 ATGACTACTCAAGGCAGATGG 377
    ||||| ||||| ||||| |||||

```

RESULT 9

A0133467

LOCUS

DEFINITION HS 3039 A2 E05 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=10 Row=I, genomic survey sequence.

ACCESSION

A0133467

VERSION

A0133467.1

GI:3524833

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

10449764

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Plate: 3039 row: I column: 10

Class: BAC ends

High quality sequence stop: 482.

Location/Qualifiers

1..482

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=3039 Col=10 Row=I"

/sex="male"

/clone_lib="CIT Approved Human Genomic Sperm Library D"

/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

E-Coli DH10B"

ORIGIN

```

Query Match      84.8%; Score 17.8; DB 8; Length 482;
Best Local Similarity 90.5%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21
    ||||| ||||| ||||| |||||
Db 161 ATGACTACTCAAGGCAGATGG 181
    ||||| ||||| ||||| |||||

```

RESULT 10

A0880134/c

LOCUS

DEFINITION HS 5037_B1_A04_T7 RPCI-11 Human Male BAC Library Homo sapiens

486 bp DNA linear GSS 09-NOV-1999

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasaki, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1445
High quality sequence stops: 332
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1446 Std Error: 0.00
Seq primer: W13RP1
High quality sequence stop: 332.
Location/Qualifiers
1..506
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:403197"
/db_xref="taxon:9606"
/clone="IMAGE:30850"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain INIB"
/note="Organ: whole brain; Vector: Lfamid BA; Site: 1: Not
1; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5',
AACTGGAGAATTCGCGCCGAGGAATTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lfamid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Patima Bonaldo."

ORIGIN

Query Match 84.8%; Score 17.8; DB 7; Length 506;
Best Local Similarity 90.5%; Pred. No. 1.le+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21
|||||
DB 291 ATGACCACAGGCAGATGG 311
|||||

RESULT 12
BI536734/C

LOCUS
BI536734
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI536734 536 bp mRNA linear EST 30-AUG-2001
396079 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
BI536734
BI536734.1 GI:153777844
EST.
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 536)
Smith.T.P.L., Grosse, W.M., Fraking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrner, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pettea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
11280013
PUBMED 11282978

TITLE
JOURNAL
MEDLINE
PUBMED

COMMENT

Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.

PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCACAGTCACGACG
 Plate: 119 row: 0 column: 2
 Seq primer: ATTAGGTGACACTATAG.

FEATURES

source
 1..536
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 4BOV"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from day 20 and day 40
 embryos."

ORIGIN

Query Match 84.8%; Score 17.8; DB 4; Length 536;
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21

DB 28 ATGACCACACAGGCAGATAG 8

RESULT 13

CE836567

LOCUS

tigr-gss-dog-17000332589366 Dog Library Canis familiaris genomic,
 genomic survey sequence.

CE836567

CE836567.1 GI:37177587

GSS:

Canis familiaris (dog)

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 543)

Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,M., Fraser,C.M. and
 Venter,J.C.

The dog genome: survey sequencing and comparative analysis

Science 301 (5641), 1898-1903 (2003)

22875432

14512627

COMMENT

Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

Location/Qualifiers

1..543

/organism="Canis familiaris"

/mol_type="Genomic DNA"

/strain="Standard Poodle"

/db_xref="taxon:9615"

/clone_lib="Dog Library"

/note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

FEATURES

source

Query Match 84.8%; Score 17.8; DB 7; Length 547;
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21

DB 372 AAGACCACACAGGTAGATGG 392

RESULT 15

BU200351/c

ORIGIN

Query Match 84.8%; Score 17.8; DB 9; Length 543;
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21

DB 367 ATGTCACATAGGCAGATGG 387

RESULT 14

CF804618

LOCUS

CF804618 547 bp mRNA linear EST 24-OCT-2003
 lad76dl1.y1 Gastric Epithelial Progenitor 2 Mus musculus cDNA 5'
 similar to SW:ROAL_BOVIN_P09867 HETEROGENEOUS NUCLEAR
 RIBONUCLEOPROTEIN A1 ; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 547)

Tidwell,R., Clifton,S., Marra,M., Hillier,L., Page,D., Martin,J.,

Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J.,

Ronko,I., Tsagareishvili,R., Belaygorod,L., Grow,A., Maguire,L.,

Waterston,R. and Wilson,R.

WashU Stem cell EST Project

Unpublished (2002)

Contact: Jeff Gordon and Mike Lovett

WashU, Human Genetics Division

Washington University School of Medicine

1st strand of cDNA was synthesized with reverse transcriptase and

oligo(dT) beads, then cDNA was amplified by PCR using modified

SMART primers. The final cDNA was cloned in pAMP1 vector in

annealing reaction with Uracil DNA Glycosylase (UDG). Library

constructed by Y.Korshunova and M. Lovett. Library materials

provided by Mills JC & Gordon JI.

Putative full length read

vector to vector length is

Seq primer: -40RP from Gibco.

Location/Qualifiers

1..547

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/tissue_type="Laser-captured isthmal cells from tox176

transgenic mice"

/dev_stage="adult"

/lab_host="DH5alpha"

/clone_lib="Gastric Epithelial Progenitor 2"

/note="Vector: pAMP1; 1st strand of cDNA was synthesized

with reverse transcriptase and oligo(dT) beads, then cDNA

was amplified by PCR using modified SMART primers. The

final cDNA was cloned in pAMP1 vector in annealing

reaction with Uracil DNA Glycosylase (UDG). Library

constructed by Y.Korshunova and M. Lovett. Library

materials provided by Mills JC & Gordon JI."

ORIGIN

Query Match 84.8%; Score 17.8; DB 7; Length 547;
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21

DB 372 AAGACCACACAGGTAGATGG 392

LOCUS BJ200351 558 bp mRNA linear EST 21-OCT-2003
DEFINITION BJ200351 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone ppn3g23 5', mRNA sequence.

ACCESSION BJ200351
VERSION BJ200351.1 GI:18368266
KEYWORDS EST.

SOURCE Physcomitrella patens subsp. patens
ORGANISM Physcomitrella patens subsp. patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariaceae; Physcomitrella.

REFERENCE 1 (bases 1 to 558)
AUTHORS Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.
TITLE Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
MEDLINE 22709184
PUBMED 12808149
COMMENT

Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-E1C phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'- GAGAGAGAGGATCCAACTGGAGTGTGTTTTTTTTTTT-3' was used as a 1st 3' primer, and 5'-ggttctcagatcgctgttcgcagacgagctgagaccggnnnn-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCAATCGCCGAGTCGAATGTCGAGACCG). cDNA instert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
 Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13- 14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCObase (<http://moss.nibb.ac.jp/>):

FEATURES

source
 1..558
 Location/Qualifiers
 /organism="Physcomitrella patens subsp. patens"
 /mol_type="mRNA"
 /sub_species="patens"
 /db_xref="taxon:145481"
 /clone="ppn3g23"
 /tissue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata"
 /clone_lib="normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN

Query Match 84.8%; Score 17.8; DB 4; Length 558;
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCACACAGGCAGATGG 21
 |||||
 Db 49 ATGACAAACACAAAGCAGATGG 29

Search completed: May 15, 2005, 14:18:45
 Job time : 100.458 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2005, 11:00:45 ; Search time 5188.09 Seconds
(without alignments)
10609.895 Million cell updates/sec

Title: US-10-764-075-1
Perfect score: 1136
Sequence: 1 aggcacgtatgggttgca.....tgataatgtagggagac 1136

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_ph.*
- 7: gb_pl.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1136	100.0	1873	14	AY534758S4
2	1136	100.0	1938	14	AY534762S6
3	1136	100.0	2810	14	AY290752
4	1136	100.0	8581	14	AY304487
5	1136	100.0	11010	14	AY304493
6	1136	100.0	11010	14	AY304494
7	1136	100.0	13471	14	AY304492
8	1136	100.0	29013	14	AY463060
9	1136	100.0	29350	14	AY394999
10	1136	100.0	29350	14	AY395000
11	1136	100.0	29350	14	AY395001
12	1136	100.0	29350	14	AY395002
13	1136	100.0	29530	14	AY394985
14	1136	100.0	29573	14	AY338174
15	1136	100.0	29573	14	AY338175
16	1136	100.0	29573	14	AY348314
17	1136	100.0	29577	14	AY559094
18	1136	100.0	29592	14	AY463059
19	1136	100.0	29620	14	AY395004

20	1136	100.0	29640	14	AY394978	AY394978	SARS	CORO
21	1136	100.0	29645	14	AY394979	AY394979	SARS	CORO
22	1136	100.0	29646	14	AY394982	AY394982	SARS	CORO
23	1136	100.0	29661	14	AY559086	AY559086	SARS	CORO
24	1136	100.0	29670	14	AY559082	AY559082	SARS	CORO
25	1136	100.0	29699	14	AY394983	AY394983	SARS	CORO
26	1136	100.0	29705	14	AY283795	AY283795	SARS	CORO
27	1136	100.0	29706	14	AY283797	AY283797	SARS	CORO
28	1136	100.0	29709	14	AY394987	AY394987	SARS	CORO
29	1136	100.0	29710	14	AY559091	AY559091	SARS	CORO
30	1136	100.0	29711	14	AY283794	AY283794	SARS	CORO
31	1136	100.0	29711	14	AY283796	AY283796	SARS	CORO
32	1136	100.0	29711	14	AY283798	AY283798	SARS	CORO
33	1136	100.0	29711	14	AY427439	AY427439	SARS	CORO
34	1136	100.0	29712	14	AY559093	AY559093	SARS	CORO
35	1136	100.0	29713	14	AY559085	AY559085	SARS	CORO
36	1136	100.0	29713	14	AY559092	AY559092	SARS	CORO
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40	1136	100.0	29716	14	AY559081	AY559081	SARS	CORO
41	1136	100.0	29716	14	AY559087	AY559087	SARS	CORO
42	1136	100.0	29716	14	AY595412	AY595412	SARS	CORO
43	1136	100.0	29719	14	AY559095	AY559095	SARS	CORO
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45	1136	100.0	29720	14	AY559096	AY559096	SARS	CORO

ALIGNMENTS

RESULT 1
AY534758S4
LOCUS AY534758S4 1873 bp RNA linear VRL 17-MAR-2004
DEFINITION SARS coronavirus Sin0409, partial sequence.
ACCESSION AY534761
VERSION AY534761.1 GI:45384968
KEYWORDS
SEGMENT 4 of 4
SOURCE SARS coronavirus Sin0409
ORGANISM SARS coronavirus Sin0409
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
REFERENCE 1 (bases 1 to 1873)
AUTHORS Lim,P.L., Kurup,A., Gopalakrishna,G., Chan,K.P., Wong,C.W., Ng,L.C., Se-Thoe,S.Y., Oon,L., Bai,X., Stanton,L.W., Ruan,Y., Miller,L.D., Vega,V.B., James,L., Ooi,P.L., Kai,C.S., Olsen,S.J., Ang,B. and Leo,Y.S.
TITLE Laboratory-acquired severe acute respiratory syndrome (SARS) - Singapore 2003
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1873)
AUTHORS Wei,C.L., Lee,C., Lin,S., Thoreau,H., Vega,V.B., Stanton,L.W. and Ruan,Y.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2004) Genome Institute of Singapore, 60, Biopolis Street, 02-01, Genome, Singapore 138672, Singapore
FEATURES
source
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/mol_type="genomic RNA"
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/country="Singapore"

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 766 CCGCAATCTTAATAACAATGCTGCCACCGTGTACAACTTCTCAAGGAACAACATTGCC 825
QY 121 AAAAGGCTTCTACGCAGAGGGAAGCAGAGCGGCAGTCAAGCCTCTTCTCGCTCCTCATC 180
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QY 361 GAAATCTGCTGTAGGCAATTAATAAGCCTCGCAAAACAGTACTGCCACAAAACAGTA 420
Db 1066 GAAATCTGCTGTAGGCAATTAATAAGCCTCGCAAAACAGTACTGCCACAAAACAGTA 1125
QY 421 CAACGCTCACTCAGCAATTTGGGAGACGTGGTCCAGAACAAACCCCAAGGAAATTCGGGA 480
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Db 1186 CCAAGACCTTAATCAGACAAAGGAACGATTACAAACATTTGGCGCGCAATTTGCAAAATTTGC 1245
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Db 1246 TCCAAGTGCCTGTGCATTTCTTGGAAATGTCAAGCATTTGGCATGGAGTCAACCTTCGGG 1305
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Db 1306 AACATGGCTGACTTATCATGGAGCCATTAAATTTGATGACAAAGATCCCAAAATTCAGAA 1365
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Db 1486 GCAGCCCACTGTGACTCTTCTCTCGCGCTGACATGGATGATTTCTCCAGACAACTTCA 1545
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Db 1546 AAATTCATGAGTGGAGCTTCTGCTGATTAACACTCAGGCATATAACACTCATGATGACCAC 1605
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QY 961 TTGTGAGATGAATTTCTCGTAACATAACAGCAGCAGTAGTGTATTAGTTAACTTTAATCTC 1020
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QY 1021 ACATAGCAATCTTTAATCAATGTGTAACTTAAAGGAGGACTTGAAGAGCCACCACATTT 1080
Db 1726 ACATAGCAATCTTTAATCAATGTGTAACTTAAAGGAGGACTTGAAGAGCCACCACATTT 1785
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Db 1786 TCATCAGGCCACGCGGAGTACGATCGAGGGTACAGTGAATTAATGCTAGGGAGAGC 1841

RESULT 2
AY53476286
LOCUS SARS coronavirus Sin_WNV, partial sequence. 1938 bp RNA linear VRL 17-MAR-2004
DEFINITION
ACCESSION AY534767
VERSION AY534767.1 GI:45384975
KEYWORDS
SEGMENT 6 of 6
SOURCE SARS coronavirus Sin_WNV
ORGANISM SARS coronavirus Sin_WNV
Virus; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
REFERENCE 1 (bases 1 to 1938)
AUTHORS Lim,P.L., Kurup,A., Gopalakrishna,G., Chan,K.P., Wong,C.W., Ng,L.C., Se-Thoe,S.Y., Oon,L., Bai,X., Stanton,L.W., Ruan,Y., Miller,L.D., Vega,V.B., James,L., Ooi,P.L., Kai,C.S., Olsen,S.J., Ang,B. and Leo,Y.S.
TITLE Laboratory-acquired severe acute respiratory syndrome (SARS) - Singapore 2003
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1938)
AUTHORS Wei,C.L., Lee,C., Lin,S., Thoreau,H., Vega,V.B., Stanton,L.W. and Ruan,Y.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2004) Genome Institute of Singapore, 60, Biopolis Street, 02-01, Genome, Singapore 138672, Singapore
FEATURES
source location/Qualifiers
1. .1938
/organism="SARS coronavirus Sin_WNV"
/mol_type="genomic RNA"
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/country="Singapore"

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGCATCGTATGGTTCGCAACTGAGGGAGCCCTTGAATACACCCAAAGACCACATTGGCAC 60
Db 732 AGGCATCGTATGGTTCGCAACTGAGGGAGCCCTTGAATACACCCAAAGACCACATTGGCAC 791
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Db 852 AAAAGGCTTCTACGCAGAGGGAAGCAGAGCGGCAGTCAAGCCTCTTCTCGCTCCTCATC 911
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Db 1092 GAAATCTGCTGTAGGCAATTAATAAGCCTCGCAAAACAGTACTGCCACAAAACAGTA 1151
QY 421 CAACGCTCACTCAGCAATTTGGGAGACGTGGTCCAGAAACCCCAAGGAAATTTGGGGA 480
Db 1152 CAACGCTCACTCAGCAATTTGGGAGACGTGGTCCAGAAACCCCAAGGAAATTTGGGGA 1211
QY 481 CCAAGACCTTAATCAGACAAAGGAACGATTACAAACATTTGGCGCGCAAAATTTGCAATTTGC 540
Db 1212 CCAAGACCTTAATCAGACAAAGGAACGATTACAAACATTTGGCGCGCAAAATTTGCAATTTGC 1271

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Oy 601 AACATGGCTACATATCATGAGGCAATTAATTTGGATGACAAAGATCCACAATTCAAAGA 660
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Db 1392 CAACGTCATATCTGTGAACAGACACATTCAGCATACAAAACATTCACCACACAGAGCC 1451
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SARS coronavirus ZJ01 isolate ZJ01b uncharacterized protein 6,
uncharacterized protein 7a, uncharacterized protein 7b,
uncharacterized protein 8a, uncharacterized protein 8b,
nucleocapsid protein, uncharacterized protein 9b, and
uncharacterized protein 9c genes, complete cds.
AY290752
AY290752.2 GI:38735509
SARS coronavirus ZJ01
SARS coronavirus ZJ01
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
1 (bases 1 to 2810)
Li, L., Wang, Z., Lu, Y., Bao, Q., Chen, S., Wu, N., Cheng, S., Weng, J.,
Zhang, Y., Yan, J., Mei, L., Wang, X., Zhu, H., Yu, Y., Zhang, M., Li, M.,
Yao, J., Lu, Q., Yao, P., Bo, X., Wo, J., Wang, S. and Hu, S.
Severe acute respiratory syndrome-associated coronavirus genotype
and its characterization
Chin. Med. J. 116 (9), 1288-1292 (2003)
2289812
14527350
2 (bases 1 to 2810)
Wang, Z.G., Li, L.J., Luo, Y., Zhang, J.Y., Wang, M.Y., Cheng, S.Y.,
Zhang, Y.J., Wang, X.M., Lu, Y.Y., Wu, N.P., Mei, L.L. and Wang, Z.X.
Molecular biological analysis of genotyping and phylogeny of severe
acute respiratory syndrome associated coronavirus
Chin. Med. J. 117 (1), 42-48 (2004)
14733771
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RESULT 3

AY290752

LOCUS

DEFINITION

SARS coronavirus ZJ01 isolate ZJ01b uncharacterized protein 6,
uncharacterized protein 7a, uncharacterized protein 7b,
uncharacterized protein 8a, uncharacterized protein 8b,
nucleocapsid protein, uncharacterized protein 9b, and
uncharacterized protein 9c genes, complete cds.

ACCESSION

AY290752

VERSION

KEYWORDS

SOURCE

ORGANISM

SARS coronavirus ZJ01
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

REFERENCE

AUTHORS

Li, L., Wang, Z., Lu, Y., Bao, Q., Chen, S., Wu, N., Cheng, S., Weng, J.,
Zhang, Y., Yan, J., Mei, L., Wang, X., Zhu, H., Yu, Y., Zhang, M., Li, M.,
Yao, J., Lu, Q., Yao, P., Bo, X., Wo, J., Wang, S. and Hu, S.

TITLE

Severe acute respiratory syndrome-associated coronavirus genotype
and its characterization

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Wang, Z.G., Li, L.J., Luo, Y., Zhang, J.Y., Wang, M.Y., Cheng, S.Y.,
Zhang, Y.J., Wang, X.M., Lu, Y.Y., Wu, N.P., Mei, L.L. and Wang, Z.X.

TITLE

Molecular biological analysis of genotyping and phylogeny of severe
acute respiratory syndrome associated coronavirus

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

3 (bases 1 to 2810)
Wang, Z., Cheng, S., Zhang, Y., Lu, Y. and Mei, L.
Direct Submission
Submitted (03-MAY-2003) Department of Microbiology, Zhejiang Center
of Disease Prevention and Control, 17 Laozheda Rd., Hangzhou,
Zhejiang 310009, China

REFERENCE

AUTHORS

TITLE

JOURNAL

4 (bases 1 to 2810)
Wang, Z., Cheng, S., Zhang, Y., Lu, Y. and Mei, L.
Direct Submission
Submitted (05-DEC-2003) Department of Microbiology, Zhejiang Center
of Disease Prevention and Control, 17 Laozheda Rd., Hangzhou,
Zhejiang 310009, China

REMARK

COMMENT

FEATURES

SOURCE

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Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCATCGTATGGTGGCACTGAGGAGCGCTTGTAATCACCAAGACCACTTGGCAC 60
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QY 421 CAACGTCACTCAAGCATTTGGGAGACGTGTGCAGAAACAAACCCAGGAAATTCGGGGA 480
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DB 2134 TCCAAGTGCCTCTGCATCTTTGGGAATGTCAGCATTTGGCATGGGAATCACACCTTCGGG 2193

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ORIGIN
Query Match
Best Local Similarity 100.0%; Score 1136; DB 14; Length 8581;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 721 TAAAAAGGACAAAAAAGAAAAAGACTGTATGAAGCTCAGCGCTTTGGCGCAGAGACAAAAGAA 780
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RESULT 4
AY304487 8581 bp RNA linear VRL 05-NOV-2003
LOCUS SARS coronavirus S213, partial genome.
DEFINITION AY304487
ACCESSION AY304487.1 GI:34492138
VERSION
KEYWORDS
SOURCE
ORGANISM
SARS coronavirus S213
SARS coronavirus S213
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
REFERENCE
1 (bases 1 to 8581)
AUTHORS
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.
Isolation and characterization of viruses related to the SARS
coronavirus from animals in southern China
Science 302 (5643), 276-278 (2003)
JOURNAL
MEDLINE 22913660
PUBMED 12958366
REFERENCE
2 (bases 1 to 8581)
AUTHORS
Guan, Y. and Zheng, B.J.
Direct Submission
TITLE
Submitted (26-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China
JOURNAL
FEATURES
Location/Qualifiers
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Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 LOCUS SARS coronavirus HKU-65806, partial genome.
 DEFINITION
 AY304493
 ACCESSION
 AY304493.1 GI:34482144
 VERSION
 KEYWORDS
 SOURCE SARS coronavirus HKU-65806
 ORGANISM SARS coronavirus HKU-65806
 Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
 REFERENCE
 1 (bases 1 to 11010)
 Guan,Y., Zheng,B.J., He,Y.Q., Liu,X.L., Zhuang,Z.X., Cheung,C.L., Luo,S.W., Li,P.H., Zhang,L.J., Guan,Y.J., Butt,K.M., Wong,K.L., Chan,K.W., Lim,W., Shortridge,K.F., Yuen,K.Y., Peiris,J.S.M. and Poon,L.L.M.
 Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China
 Science 302 (5643), 276-278 (2003)
 JOURNAL
 MEDLINE 22913660
 PUBMED 12958366
 REFERENCE
 2 (bases 1 to 11010)
 Guan,Y. and Zheng,B.J.
 Direct Submission
 TITLE
 Submitted (27-MAY-2003) Microbiology, The University of Hong Kong, University Pathology Building, Queen Mary Hospital, Pokfulam Road, Hong Kong, China
 FEATURES
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ORIGIN

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DEFINITION SARS coronavirus HKU-66078, partial genome.
ACCESSION AY304494
VERSION AY304494.1 GI:34482145
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KEYWORDS

SARS coronavirus HKU-66078

SOURCE

SARS coronavirus HKU-66078

ORGANISM

Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;

Coronaviridae; Coronavirus.

1 (bases 1 to 11010)

Guan, Y., Zheng, B.J., He, Y.O., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,

Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,

Chan, K.W., Lim, W., Shorridge, K.F., Yuen, K.Y., Peiris, J.S.M. and

Poon, L.L.M.

Isolation and characterization of viruses related to the SARS

coronavirus from animals in southern China

Science 302 (5643), 276-278 (2003)

22913660

12958366

REFERENCE

2 (bases 1 to 11010)

AUTHORS

Guan, Y. and Zheng, B.J.

TITLE

Direct Submission

JOURNAL

Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China

FEATURES

source

Location/Qualifiers
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DEFINITION SARS coronavirus HKU-36871
ACCESSION AY304492
VERSION AY304492.1 GI:34482143
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SOURCE SARS coronavirus HKU-36871
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
REFERENCE 1 (bases 1 to 13471)
AUTHORS Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Burt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.
TITLE Isolation and characterization of viruses related to the SARS
coronavirus from animals in southern China
JOURNAL Science 302 (5643), 276-278 (2003)
MEDLINE 22913660
PUBMED 12958366
REFERENCE 2 (bases 1 to 13471)
AUTHORS Guan, Y. and Zheng, B.J.
TITLE Direct Submission
JOURNAL Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China
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DEFINITION SARS coronavirus ShanghaiQXC2, complete genome.
ACCESSION AY463060
VERSION AY463060.1 GI:40457448
KEYWORDS SARS coronavirus ShanghaiQXC2
SOURCE SARS coronavirus ShanghaiQXC2
ORGANISM

Viruses: ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 29013)
Yuan, Z., Zhang, X., Hu, Y., Lan, S., Zhou, Z., Wang, H. and Wen, Y.
Analysis of SARS coronavirus genome in Shanghai isolates
Unpublished
2 (bases 1 to 29013)
Yuan, Z., Zhang, X., Hu, Y., Lan, S., Zhou, Z., Wang, H. and Wen, Y.
Direct Submision
Submitted (11-Nov-2003) Key Lab of Medical Molecular Virology,
Shanghai Medical College, Fudan University, 138 Yi Xue Yuan Road,
Shanghai 200032, P.R. China
Location/Qualifiers

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CDS

FEATURES
source

REFERENCE
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JOURNAL

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JOURNAL		Submitted (19-SEP-2003) Guangdong, China
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TITLE	The SARS epidemiology consortium of Guangdong				
JOURNAL	From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus				
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REFERENCE 1 (bases 1 to 29350)
AUTHORS The SARS epidemiology consortium of Guangdong
CONSRMT
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TITLE From independent foci of epidemic outbreak to large genomic
JOURNAL alteration in late phase viruses: evolution of the SARS-coronavirus
REFERENCE Unpublished
2 (bases 1 to 29350)
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CONSRMT Direct Submission
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VERSION AY395002.1 GI:37624345
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SOURCE SARS coronavirus LC5
ORGANISM SARS coronavirus LC5
REFERENCE 1 (bases 1 to 29350)
AUTHORS The SARS epidemiology consortium of Guangdong
CONSTRM From independent foci of epidemic outbreak to large genomic
TITLE alteration in late phase viruses: evolution of the SARS-coronavirus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 29350)
AUTHORS The SARS epidemiology consortium of Guangdong
CONSTRM Direct Submission
TITLE Submitted (19-SEP-2003) Guangdong, China
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DEFINITION SARS coronavirus HSZ-Bb, complete genome.
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SOURCE SARS coronavirus HSZ-Bb
ORGANISM SARS coronavirus HSZ-Bb
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REFERENCE	1	(bases 1 to 29530)	
AUTHORS		The SARS epidemiology consortium of Guangdong	
CONSTRM		From independent foci of epidemic outbreak to large genomic	
TITLE		alteration in late phase viruses: evolution of the SARS-coronavirus	
JOURNAL		Unpublished	
REFERENCE	2	(bases 1 to 29530)	
AUTHORS		The SARS epidemiology consortium of Guangdong	
CONSTRM		Direct Submission	
TITLE		Submitted (19-SEP-2003) Guangdong, China	
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ACCESSION	AY338175				
VERSION	AY338175.1	GI:32493130			
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SOURCE	SARS coronavirus Taiwan TC2				
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.				
REFERENCE	1 (bases 1 to 29573)				
AUTHORS	Chang, J., Lin, T., Chen, C., Lin, T., Chan, W. and Shih, M.				
TITLE	SARS coronavirus TC2, clinical specimen				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 29573)				
AUTHORS	Chang, J., Lin, T., Chen, C., Lin, T., Chan, W. and Shih, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-JUL-2003) Department of Molecular Medicine, China Medical University Hospital, 2, Yuh Der Road, Taichung, Taichung 404, Taiwan				
REFERENCE	3 (bases 1 to 29573)				
AUTHORS	Chang, J., Lin, T., Chen, C., Lin, T., Chan, W. and Shih, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (28-JUL-2003) Department of Molecular Medicine, China Medical University Hospital, 2, Yuh Der Road, Taichung, Taichung 404, Taiwan				
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CDS					

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	42	3.7	2000	8	ABX14055 Mouse POZ
4	41.8	3.7	7359	6	ABL33863 Human imm
5	40.4	3.6	463	8	ABL14053 Mouse pox
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7	40.2	3.5	2543	6	ABQ33612 Oligonuc
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9	39.2	3.5	9830	6	ABL70196 Chemical
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ALIGNMENTS

RESULT 1

ADJ39000

ID ADJ39000 standard; DNA; 29751 BP.

XX AC ADJ39000;

XX DT 06-MAY-2004 (first entry)

XX DE SARS coronavirus nucleotide sequence.

XX KW small interfering RNA; siRNA; modified ribonucleotide;

XX KW viral replication inhibition; hepatitis C virus; HCV; hepatitis C;

XX KW antinflammatory; hepatotropic; virucide; hepatitis A virus;

XX KW hepatitis D virus; hepatitis E virus; Ebola virus; influenza virus;

XX KW rotavirus; reovirus; retrovirus; poliovirus; human papilloma virus;

XX KW metapneumovirus; coronavirus; viral infection; gene; ds.

XX OS SARS coronavirus.

XX PN WO2004011647-A1.

XX PD 05-FEB-2004.

XX PF 25-JUL-2003; 2003WO-US023104.

XX PR 26-JUL-2002; 2002US-0398605P.

XX PA (CHIR) CHIRON CORP.

XX PI Han J, Seo MY, Houghton M;

XX DR WPI; 2004-143862/14.

XX PT New RNase resistant small interfering RNA, useful for treating viral

XX PT infections, e.g., hepatitis C, influenza virus or coronavirus infection.

XX PS Example 10; Fig 3; 74pp; English.

XX CC The present invention describes a small interfering RNA (siRNA) which

XX CC comprises a modified ribonucleotide, where the siRNA is resistant to

XX CC RNase and retains the ability to inhibit viral replication. Also

XX CC described: (1) inactivating a virus in a patient; (2) making a modified

XX CC siRNA that targets a nucleic acid sequence in a virus; (3) a double-

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C	24	37	3.3	551	13	ACN55746	ACN55746 Cotton an
C	25	36.8	3.2	704	5	AAF93473	Aaf93473 cDNA enco
C	26	36.4	3.2	652	6	ABQ30525	Abq30525 Oligonuc
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C	30	36.4	3.2	5557	6	ABL33547	AbL33547 Human imm
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C	44	35.8	3.2	505	8	ABZ36661	Abz36661 Human GEN
C	45	35.8	3.2	713	4	AAI60951	Aai60951 Human pol

stranded RNA molecule of 10-30 nucleotides that inhibits replication of hepatitis C virus (HCV); (4) inducing targeted RNA interference toward HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector comprising a DNA segment encoding the RNA molecule; (7) a host cell comprising the vector of (6); (8) inhibiting replication of HCV in cells carrying HCV; (9) treating hepatitis C in a subject; (10) a modified siRNA molecule comprising a double-stranded RNA molecule of 10-30 nucleotides in length, which mediates RNA interference toward a target agent or virus and is linked to at least one receptor-binding ligand; and (11) inducing targeted RNA interference in a patient. The modified siRNA molecules have antiinflammatory, hepatotropic and virucide activities. The modified RNA molecules are useful for inactivating virus in mammalian cells. The siRNAs are useful for treating hepatitis C virus, hepatitis A virus, hepatitis D virus, hepatitis E virus, Ebola virus, influenza virus, rotavirus, reovirus, retrovirus, poliovirus, human papilloma virus, metapneumovirus or coronavirus infections. The methods of the invention can be used to correct or compensate for cellular physiological abnormalities involved in conferring susceptibility to viral infections in patients and/or alleviate symptoms of a viral infection in patients. The present sequence represents the SARS coronavirus nucleotide sequence, which is used in an example from the present invention.

Query Match 100.0%; Score 1136; DB 12; Length 29751; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0; Matches 1136; Conservative 0; Indels 0

1 AGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACCCCAAGACCACATTGGCAC 60
28506 AGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACCCCAAGACCACATTGGCAC 28505

61 CCGCAATCTTAATACATGTCGCCCGTGTCAAACTTCTCAAGGAACAACTTGGC 120
28566 CCGCAATCTTAATACATGTCGCCCGTGTCAAACTTCTCAAGGAACAACTTGGC 28625

121 AAAAGGCTTACGAGAGGGAAGCAGAGGGCGGAGTCAAGCTCTTTCGCTCCCTCATC 180
28626 AAAAGGCTTACGAGAGGGAAGCAGAGGGCGGAGTCAAGCTCTTTCGCTCCCTCATC 28695

181 AGCTAGTCGCGTAATTCAGAAATTCAACTCTCGCAGCAGTAGGGGAAATTCCTCTGC 240
28686 AGCTAGTCGCGTAATTCAGAAATTCAACTCTCGCAGCAGTAGGGGAAATTCCTCTGC 28745

241 TCGAATGGCTACGGAGGTGGTGAATCGCCCTCGCGCTATTTGCTGTAGACAGATTGAA 300
28746 TCGAATGGCTACGGAGGTGGTGAATCGCCCTCGCGCTATTTGCTGTAGACAGATTGAA 28805

301 CCAGCTTCGAGAGCAAGTTTCTGTTAAAGGCCAACAAAGGCCAAACTGTCTCACTAA 360
28806 CCAGCTTCGAGAGCAAGTTTCTGTTAAAGGCCAACAAAGGCCAAACTGTCTCACTAA 28865

361 GAAATCTGCTGCTGAGGCATCTAAAAGCCTCGCCAAAACGTAAGTCCACAAAACAGTA 420
28866 GAAATCTGCTGCTGAGGCATCTAAAAGCCTCGCCAAAACGTAAGTCCACAAAACAGTA 28925

421 CAACTGCTACTAAGCATTTGGAGACGTGGTCCAGAAACAAAGGAAATTTTCGGGA 480
28926 CAACTGCTACTAAGCATTTGGAGACGTGGTCCAGAAACAAAGGAAATTTTCGGGA 28985

481 CCAAGACCTTAATCAGACAGGAACGTATTACAAACATTGGCCGCAAAATTCGCAATTTGC 540
28986 CCAAGACCTTAATCAGACAGGAACGTATTACAAACATTGGCCGCAAAATTCGCAATTTGC 29045

541 TCCAAAGTGCCTCTGCAATCTTTGGAAATGTACGCAATTTGGCATGGGAATCACACCTTCGGG 600
29046 TCCAAAGTGCCTCTGCAATCTTTGGAAATGTACGCAATTTGGCATGGGAATCACACCTTCGGG 29105

601 AACATGGCTGACTTATCATGGAGCCATTTAAATTTGGATGACAAAGATCCCAATTCAGAA 660
29106 AACATGGCTGACTTATCATGGAGCCATTTAAATTTGGATGACAAAGATCCCAATTCAGAA 29165

661 CAACTGCATCTGCTGAAACAGCACATTTGACGCATACAAACATTTCCCAACCAACAGAGCC 720

||||| 29166 CAACGTATATCTGCTGACACAGCAGCATTTGACGCATACAAAACATTTCCCAACACAGAGCC 29225
QY 721 TAAAAAGGACAAAAAGAAAAAGAGATGATGAAGCTCAGCCTTTGCGCGAGAGACAAAAAGAA 780
Db 29226 TAAAAAGGACAAAAAGAAAAAGAGATGATGAAGCTCAGCCTTTGCGCGAGAGACAAAAAGAA 29285
QY 781 GCAGCCCACTGTGACTCTTCTTCCTGCGGCTGACATGATGATTTCTCCAGACACTTCA 840
Db 29286 GCAGCCCACTGTGACTCTTCTTCCTGCGGCTGACATGATGATTTCTCCAGACACTTCA 29345
QY 841 AAATTTCCATGATGAGCTTCTGCTGATTCAACTCAGGCATAAAACACTCATGATGACCCAC 900
Db 29346 AAATTTCCATGATGAGCTTCTGCTGATTCAACTCAGGCATAAAACACTCATGATGACCCAC 29405
QY 901 ACAAGGCAGATGGGCTATGTAACGTTTTTCGCAATTCGTTTACGATACATGCTACTC 960
Db 29406 ACAAGGCAGATGGGCTATGTAACGTTTTTCGCAATTCGTTTACGATACATGCTACTC 29465
QY 961 TTGTGCAAGATGAATTTCTCGTAACTTAAACAGCACAAGTAGTTTAACTTTAATCTC 1020
Db 29466 TTGTGCAAGATGAATTTCTCGTAACTTAAACAGCACAAGTAGTTTAACTTTAATCTC 29525
QY 1021 ACATAGCAATCTTTAATCAATGTGTAACTTAGGGAGGACTTTGAAAGAGCCACCACTTT 1080
Db 29526 ACATAGCAATCTTTAATCAATGTGTAACTTAGGGAGGACTTTGAAAGAGCCACCACTTT 29585
QY 1081 TCATCGAGGCCACCGGAGTACGATCGAGGGTACAGTGAATTAATCTTAGGGAGAGC 1136
Db 29586 TCATCGAGGCCACCGGAGTACGATCGAGGGTACAGTGAATTAATCTTAGGGAGAGC 29641

RESULT 2
ADA71938
ID ADA71938 standard; DNA; 2000 BP.
XX
AC ADA71938;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 5263.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 27; SEQ ID NO 5263; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to


```

DT 12-JUL-2002 (first entry)
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 30204.
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
XX Homo sapiens.
XX WO200218632-A2.
XX 07-MAR-2002.
XX 01-SEP-2001; 2001WO-EP010074.
XX 01-SEP-2000; 2000DE-01043826.
XX 05-SEP-2000; 2000DE-01044543.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX Determining the degree of cytosine methylation in genomic DNA, useful for
XX diagnosis and prognosis, comprises selective hybridization of amplicons
XX from chemically treated DNA.
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one member,
XX of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
XX degree of hybridisation to both classes is determined from the label on
XX the amplicon. From the ratio of labels hybridised to the two classes of
XX oligomers, the degree of methylation is calculated. The method is used:
XX (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
XX and of a wide range of diseases, e.g. cancer, disorders of the central
XX nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
XX particularly by detecting mutations or single nucleotide polymorphisms
XX (SNP's); and (ii) for differentiation of cell or tissue types and for
XX investigating cell differentiation. The method allows the methylation
XX status of many C residues to be determined simultaneously. ABQ13410-
XX CC ABQ54121 represent genomic DNA sequences used to illustrate the method
XX for determining the degree of cytosine methylation described in the
XX disclosure of the invention
XX SQ Sequence 2543 BP; 1529 A; 616 C; 230 G; 168 T; 0 U; 0 Other;
Query Match 3.5%; Score 40.2; DB 6; Length 2543;
Best Local Similarity 59.0%; Pred. No. 0.52;
Matches 69; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 629 AAATTGGATGACAAAGATCCACATTTCAAAGACAACGTCATCTGCTGAACAGCACATT 688
DB 28 AAAAAAACCCAAAAACGCAAAAAATAAATAAAGCGCAATAAATAAAGCGCAAAAAA 87
QY 689 GAGCGCATACAAAACATTTCCCAACCAACAGAGCCTTAAAGAGGACAAAAAGAAAGACT 745
DB 88 AACGCCACGAAACACACCGAAAAAACCAGCAAAAAAACCACTAAAAAANAAT 144
RESULT 7
ABQ43612/C
ID ABQ43612 standard; DNA; 2543 BP.
XX ABQ43612;

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XX 12-JUL-2002 (first entry)
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 30203.
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
XX Homo sapiens.
XX WO200218632-A2.
XX 07-MAR-2002.
XX 01-SEP-2001; 2001WO-EP010074.
XX 01-SEP-2000; 2000DE-01043826.
XX 05-SEP-2000; 2000DE-01044543.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX Determining the degree of cytosine methylation in genomic DNA, useful for
XX diagnosis and prognosis, comprises selective hybridization of amplicons
XX from chemically treated DNA.
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one member,
XX of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
XX degree of hybridisation to both classes is determined from the label on
XX the amplicon. From the ratio of labels hybridised to the two classes of
XX oligomers, the degree of methylation is calculated. The method is used:
XX (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
XX and of a wide range of diseases, e.g. cancer, disorders of the central
XX nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
XX particularly by detecting mutations or single nucleotide polymorphisms
XX (SNP's); and (ii) for differentiation of cell or tissue types and for
XX investigating cell differentiation. The method allows the methylation
XX status of many C residues to be determined simultaneously. ABQ13410-
XX CC ABQ54121 represent genomic DNA sequences used to illustrate the method
XX for determining the degree of cytosine methylation described in the
XX disclosure of the invention
XX SQ Sequence 2543 BP; 168 A; 230 C; 616 G; 1529 T; 0 U; 0 Other;
Query Match 3.5%; Score 40.2; DB 6; Length 2543;
Best Local Similarity 59.0%; Pred. No. 0.52;
Matches 69; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 629 AAATTGGATGACAAAGATCCACATTTCAAAGACAACGTCATCTGCTGAACAGCACATT 688
DB 2516 AAAAAAACCCAAAAACGCAAAAAATAAATAAAGCGCAATAAATAAAGCGCAAAAAA 2457
QY 689 GAGCGCATACAAAACATTTCCCAACCAACAGAGCCTTAAAGAGGACAAAAAGAAAGACT 745
DB 2456 AACGCCACGAAACACACCGAAAAAACCAGCAAAAAAACCACTAAAAAANAAT 2400
RESULT 8
ABK31241/C
ID ABK31241 standard; DNA; 9830 BP.
XX

```

AC ABK31241;
XX
DT 23-APR-2002 (first entry)
XX
DE
XX
XX Signal transduction associated gene modified complementary DNA #42.
XX
KW Human; signal transduction associated gene; cytosine methylation state;
KW CpG island; signal transduction associated disease; solid tumour; cancer;
KW antitumour; cytostatic; mutant; ds.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200200926-A2.
FN
XX
XX 03-JAN-2002.
PD
XX
XX 29-JUN-2001; 2001WO-EP007472.
XX
XX 30-JUN-2000; 2000DE-01032529.
PR
XX 01-SEP-2000; 2000DE-01043826.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2002-147896/19.
DR
XX
XX Oligonucleotide for diagnosis and therapy of diseases associated with
PT signal transduction e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with signal transduction.
PT
XX
PS Claim 1; SEQ ID NO 84; 24pp; English.
XX
XX The present invention relates to chemically modified DNA sequences of
CC signal transduction associated genes. The DNA sequences are chemically
CC modified using a solution of bisulphite, hydrogen sulphite or disulphite.
CC Also disclosed are oligonucleotides and/or PNA oligomers for detecting
CC the cytosine methylation state (CpG islands) of these genes, and a method
CC for the diagnosis and/or therapy of genetic and epigenetic parameters of
CC genes associated with signal transduction. The genomic DNA can be
CC obtained from cells or cellular components which contain DNA, e.g. cell
CC lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid,
CC tissue embedded in paraffin such as tissue from eyes, intestine, kidney,
CC brain, heart, prostate, lung, breast or liver, histologic object slides,
CC and all their possible combinations. The sequences of the invention are
CC useful for the diagnosis and therapy of diseases associated with signal
CC transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent
CC chemically pretreated genomic DNA sequences of different genes associated
CC with signal transduction, or their complementary sequences. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office
XX
SQ Sequence 9830 BP; 2285 A; 267 C; 2773 G; 4505 T; 0 U; 0 Other;

Query Match 3.5%; Score 39.2; DB 6; Length 9830;
Best Local Similarity 52.4%; Pred. No. 2;
Matches 86; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 639 ACAAGATCCCAATTCAAGACACGTCATCTACTGCTGAACAGCACATTGACGATACA 698
|||
Db 6121 ACACCAAAACGAAACCAAAATATCCATCCGACAAAAAACCACGCTACCTAAATA 6062
|||
QY 699 AAACATTTCCACCAACAGAGCCTTAAAGGACAAAGGACAAAGAAAGACTGTAGAGCTCAGC 758
|||
Db 6061 ACAATCCCGACATCAAAACGAAATATAAATCAAAAAAATAAATAAACAATAAAT 6002
|||
QY 759 CTTTCCCGCAGACAGACAAAGAGCAGCCACCTGTGACTCTTCTT 802
|||
Db 6001 CTAATAACCTCCCAAAAAATCAAAACCTTACCACAAATTACTCTTCTT 5958
|||

RESULT 9
ABL70196/c
ID ABL70196 standard; DNA; 9830 BP.
XX
AC ABL70196;
XX
DT 01-JUL-2002 (first entry)
XX
DE Chemically treated cell signalling DNA sequence complementary to#43.
XX
XX Cell signalling; cytosine methylation; cell signalling disease; cancer;
KW tumour; cytostatic; ds.
XX
XX Unidentified.
OS
XX WO200202807-A2.
FN
XX
XX 10-JAN-2002.
PD
XX
XX 29-JUN-2001; 2001WO-EP007471.
XX
XX 30-JUN-2000; 2000DE-01032529.
PR
XX 01-SEP-2000; 2000DE-01043826.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2002-154758/20.
DR
XX
XX Nucleic acid, useful for diagnosis and therapy of diseases associated
PT with cell signaling e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with cell signaling.
PT
XX
PS Claim 1; SEQ ID NO 86; 24pp + Sequence Listing; English.
XX
XX The invention relates to a nucleic acid comprising a sequence of at least
CC 18 bases of a segment of chemically pretreated DNA of genes associated
CC with cell signaling. The activity of the modified sequences of the
CC invention may be described as cytostatic. The object of the invention is
CC to provide the chemically modified DNA of genes associated with cell
CC signalling, as well as oligonucleotides and/or PNA-oligomers for
CC detecting cytosine methylations, as well as a method which is
CC particularly suitable for the diagnosis and/or therapy of genetic and
CC epigenetic parameters of genes associated with cell signalling. The
CC chemically modified DNA provided by the invention is useful for diagnosis
CC and therapy of diseases such as solid tumours and cancer. The sequences
CC given in records ABL70111-ABL70626 represent chemically pre-treated
CC genomic DNA's of genes associated with cell signalling. Note: The
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office
XX
SQ Sequence 9830 BP; 2285 A; 267 C; 2773 G; 4505 T; 0 U; 0 Other;

Query Match 3.5%; Score 39.2; DB 6; Length 9830;
Best Local Similarity 52.4%; Pred. No. 2;
Matches 86; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 639 ACAAGATCCCAATTCAAGACACGTCATCTACTGCTGAACAGCACATTGACGATACA 698
|||
Db 6121 ACACCAAAACGAAACCAAAATATCCATCCGACAAAAAACCACGCTACCTAAATA 6062
|||
QY 699 AAACATTTCCACCAACAGAGCCTTAAAGGACAAAGGACAAAGAAAGACTGTAGAGCTCAGC 758
|||
Db 6061 ACAATCCCGACATCAAAACGAAATATAAATCAAAAAAATAAATAAACAATAAAT 6002
|||
QY 759 CTTTCCCGCAGACAGACAAAGAGCAGCCACCTGTGACTCTTCTT 802
|||
Db 6001 CTAATAACCTCCCAAAAAATCAAAACCTTACCACAAATTACTCTTCTT 5958
|||

[illegible]

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QY 639 ACAAGATCCACAATTCAAGACACGTCATCTGCTGAAACAGCACATTGACGCATACA 698
D 6121 ACACCAAAACGAAAAACCAAAATATCCACATCCGACCAAAAAAACCACCGTACCTAAATA 6062
QY 699 AAACATTCCTCCACACAGAGCGCTAAAAAGGACAAAAAGAAAAAGAACTGATGAAGCTCAGC 758
D 6061 ACAATATCCGACATCAAAACGAAATTAATCAAAAAAATAAACAATAAACAATAAAT 6002
QY 759 CTTTCCCGCAGACAGACAAAGAGCAGCCACTGTGACTCTTCTT 802
D 6001 CTAAAACTCCCAAAATCAAACTACCAACAATTACTCTTCTT 5958

RESULT 12
ABV57028
ID ABV57028 standard; cDNA; 481 BP.
XX
AC ABV57028;
XX
DT 17-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 57019.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US0051171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 10980; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 481 BP; 204 A; 82 C; 48 G; 145 T; 0 U; 2 Other;

Query Match 3.4%; Score 39; DB 5; Length 481;
Best Local Similarity 49.3%; Pred. NO. 0.54;
Matches 99; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
```

```
QY 589 CACACCTCCGGGAACATGGCTGACTTATCATCGAGCCATTAAATTTGGATGACAAGATCC 648
D 7 CCCCCCTCGGGTACTTCTAGNATTATTAACGCGGATTTTAAAGAAAGAAAAAAGAAC 66
QY 649 ACAATTCACAGACAAACGTCATCTGCTGAAACAAGCACATTCGCGCATACAAAAACATTCCC 708
D 67 AAAAAAACAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 126
QY 709 ACCACACAGAGCTAAAGAGCAAAAGAGAAAAAGAAAGAACTGATGAAGCTCAGCCTTTGCCGCA 768
D 127 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAATTTTAAA 186
QY 769 GAGACAAAAGAGAGCAGCCAC 789
D 187 AAAAAAAGAGCCGCCCC 207

RESULT 13
ADQ24871
ID ADQ24871 standard; DNA; 5284 BP.
XX
AC ADQ24871;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7691.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW ds.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
WPI; 2004-441208/41.
XX
DR Early detection of soft tissue sarcoma comprises determining expression
DR of a gene in a first soft tissue sample and a normal soft tissue sample
DR and comparing the gene expression, also useful in treating soft tissue
DR sarcoma.
XX
PS Example 2; SEQ ID NO 7691; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method for detecting soft tissue
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 5284 BP; 1397 A; 1242 C; 1236 G; 1377 T; 0 U; 32 Other;

Query Match 3.4%; Score 39; DB 12; Length 5284;
Best Local Similarity 54.4%; Pred. NO. 1.7;
Matches 98; Conservative 0; Mismatches 81; Indels 1; Gaps 1;
```

565	GTCTACACATGGAGAATAATANCCTAGTTGACAAAAGCCANTTTAAGCAAGACATCTGC	AA	624
670	ACTGCTGAACAAGCACATTTGACGCATACAAAACATTTCCACCAACAGAGCCTAAAAA	AG	729
625	TCCTCANCATGACATTTGACTTTTAAATCACAGCCCAANGGACAACACTCCTCTAA	ATTC	684
730	CAAAAGAAAAGACTGATGAAGCTCAGCCTTTGGCCGACAGACACAAAAGAGAGCC	CCAC	789
685	TAAAGACAAACGGAAATANTTAAATTTCTGCAACCCNCAAAAAAAAATTCACAG	GCANAA	744
790	TGTGACTCTCTCTCC		804
745	ATTGGGTTTTTTTCC		759

RESULT 15
ADAY1938/c
ID ADA71938 standard; DNA; 2000 BP.
XX
XX AC ADA71938;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE Rice gene, SEQ ID 5263.
XX
XX KW Plant; bacterial infection; fungal infection; viral infection; rice;
XX gene; ds.
XX
XX OS Oryza sativa.
XX
XX PN WC2003000898-A1.
XX
XX PD 03-JAN-2003.
XX
XX PF 22-JUN-2001; 2001WO-IB001105.
XX
XX PR 22-JUN-2001; 2001WO-IB001105.
XX
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
XX DR WPI: 2003-175290/17

XX
DR
XX
PT
PT
PT
PT
PT

WPI; 2003-175290/17.

Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.

XX Claim 27; SEQ ID NO 5263; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes
XX involved in plant resistance or response to pathogenic infection. M1
XX comprises identifying a gene whose expression is significantly altered in
XX the incompatible interaction of plant gene expression relative to
XX expression of the gene in an uninfected plant, in a mutant plant that
XX does not express a gene associated with response to pathogenic infection,
XX or in a corresponding incompatible or compatible interaction. (M1) is
XX useful for conferring resistance to resistance or tolerance to a plant to
XX bacterial, fungal or viral infection. The present sequence was used to
XX illustrate the invention.

Query Match 3.4%; Score 38.6; DB 8; Length 2000;
Best Local Similarity 10.2%; Pred.No. 1.4;

QY	314	AAAGTTTCTGGTAAAGGCCAACACAAAGGCCAAACTGTCACTAAGAAATCTGCTGCT	373
Matches	67	Conservative 299; Mismatches 278; Indels 11; Gaps	

Db 853 MWRYTMYTYCYAMTCAKCKYKNAMTKWTTWACAWRATSWRWRAMAGMRWKRYOMKRAY 794

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2005, 11:11:51 ; Search time 249.39 Seconds
(without alignments)
7453.434 Million cell updates/sec

Title: US-10-764-075-1
Perfect score: 1136
Sequence: 1 aggcacgtatgggttgcac.....tgaataatgtagggagagc 1136

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	43	3.8	1141	4	US-09-806-708B-22
C 2	39.4	3.5	2889	4	US-09-248-796A-5056
C 3	38.6	3.4	7218	1	US-08-232-463-14
C 4	37.4	3.3	13489	4	US-09-949-016-15911
C 5	36	3.2	601	4	US-09-949-016-53337
C 6	36	3.2	110402	4	US-09-949-016-17295
C 7	36	3.2	110403	4	US-09-949-016-12741
C 8	36	3.2	139936	4	US-09-949-016-11782
C 9	36	3.2	139952	4	US-09-949-016-13280
C 10	35.8	3.2	1450	4	US-09-620-312D-1058
C 11	35.8	3.2	1862	3	US-09-336-643A-11
C 12	35.6	3.1	601	4	US-09-949-016-53338
C 13	34.8	3.1	601	4	US-09-949-016-102602
C 14	34.8	3.1	601	4	US-09-949-016-102714
C 15	34.8	3.1	6755	3	US-08-931-999-4
C 16	34.8	3.1	678533	4	US-09-949-016-14577
C 17	34.8	3.1	678533	4	US-09-949-016-14578
C 18	34.6	3.0	320	4	US-09-621-976-2771
C 19	34.6	3.0	326	4	US-09-513-999C-10231
C 20	34.6	3.0	345	4	US-09-513-999C-10233
C 21	34.6	3.0	423	4	US-09-621-976-2768
C 22	34.6	3.0	424	4	US-09-621-976-2767
C 23	34.6	3.0	436	4	US-09-621-976-2766
C 24	34.6	3.0	504	4	US-09-621-976-16332
C 25	34.6	3.0	556	4	US-09-621-976-2769
C 26	34.6	3.0	1278	3	US-09-134-001C-2817
C 27	34.6	3.0	2175	4	US-09-710-279-967

ALIGNMENTS

RESULT 1

US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAEl promoters
US-09-806-708B-22

Query Match	3.8%;	Score 43;	DB 4;	Length 1141;
Best Local Similarity	11.7%;	Pred. No. 0.0059;		
Matches	36;	Conservative 142;	Mismatches 130;	Indels 1; Gaps 1;
Qy	739	AAAGACTGATGAAGCTCAGCCTTGGCGCAGACAGAAAGAGAGCCACTGTGACTCT	798	
Db	451	MMRRRAKMMMAWCCRRAYCCNNNNRACVWHKHMMRWTKYMKWKAACNNNNBKANYMR	392	
Qy	799	TCTTCCTCGCGCTGACATGGATGATTCTCCAGACAACTTCAAAATTCATGAGTGGAGC	858	
Db	391	VAMMYSRDITNTDMMWTSDBWHWYTDYTWRAWNNNNNNNNNRBCKTTSWMMWMDHM	332	
Qy	859	TTCTGCTGATTCAACTCAGCATAAACAATCATGATGACCAACAGGCGAGATGGGTAT	918	
Db	331	NTHCTYGNNTWGSAYEMAAMSMWAAGASNBVTYNNCWMMTYMGKTMNTNNNNNKAWYRT	272	
Qy	919	GTAACCTTTTCGCAATTCGGTTTACGAT-ACATAGTCTACTCTTGTCGAGAATGAATTC	977	
Db	271	KTVAMCNRYYDTAVMTXRNKYCYAVBYWYBYMYGKHWHWRBHRBHSWNNWVKC	212	
Qy	978	TCGTAACCTAACACACAGTAGGTTTAACTTAACTCTCACAATAGCAATCTTTAAT	1037	
Db	211	RNKYMYSHVHYMBRYBKWABAVGCCNNWKKDRMAHHHWCATNNNNNNWWWYATMHHMKKGK	152	
Qy	1038	CAATGTGTA	1046	


```
; ORGANISM: Human
US-09-949-016-15911

Query Match      3.3%; Score 37.4; DB 4; Length 13489;
Best Local Similarity 52.2%; Pred. No. 1.6; Mismatches 0; Gaps 0;
Matches 83; Conservative

QY 583 GGAAGTCACACCTTCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAA 642
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11661 GGAAGTAACACGCTGCGCACGAGTTGACTTTTAAATTTGCTTAAAGCGCTGAAGCAA 11602
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 643 AGATCCACATTTCAAGACAACTCATCTGCTGGAACAGCACATTTGACCATACAAAAC 702
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11601 AAACCATGATAAACACATTTCTGCTTTCTTTTACACCCCAAGCAACGCAAAAAAAA 11542
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 703 ATTCCCAACCAACAGAGCCTTAAAGGACAAAAAGAAAA 741
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11541 AAAAAAACAACAACAACAACAACAACAACAACAACA 11503
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
US-09-949-016-53337
; Sequence 53337, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53337
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-53337

Query Match      3.2%; Score 36; DB 4; Length 601;
Best Local Similarity 54.5%; Pred. No. 0.7; Mismatches 60; Indels 0; Gaps 0;
Matches 72; Conservative

QY 326 AAAGGCCAACAAACAAGCCCAAACTGTCACTTAAGAAATCTGCTGAGGCACTTAAA 385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 AAGAGTCATACCCTGTAAGCCACCATTTCAGCAGAGACAAACAAGACCCCTCAAC 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 386 AAGCTTCGCAAAAACGTACTGCGCAAAAACAGTACAAAGTCACTCAAGCATTTGGAGA 445
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 AAGCAAGGCACTGAAAGTACTGAATCAAACTTAAAGCACTCACAGGCAAAAGGAAAA 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 446 CGTGTCCAGAA 457
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 124 CATGGTACAAAA 135
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
US-09-949-016-17295/c
; Sequence 17295, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17295
; LENGTH: 110403
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17295

Query Match      3.2%; Score 36; DB 4; Length 110403;
Best Local Similarity 50.4%; Pred. No. 16; Mismatches 110; Indels 2; Gaps 1;
Matches 114; Conservative

QY 652 ATTCAAAGACAACGTCATCTGCTGAACAAGCACATTTGACGCATACAAAACATTCCACC 711
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16399 ATATATATATATACACATATATACACACACACATCTATCTTATTAAATTTCTCCCTCT 16340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 712 AACAGAGCCTTAAAGGACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 771
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16339 AGAGAAACCCCTAATACATATACACAAAATTTCTTAACCCAAAAGTGTTTAGTGAAGAA 16280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 772 ACAAAGAAAGCAGCCCACTGTGACTCTTCTCTCGCGGCTGACATGATGATTTCTCCAG 831
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16279 ATACGAGAGAGTGTAAATGCTACTCT--TTCTGAGGCTGACAAAGACAAAGACAAGTA 16222
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 832 ACAACTTCAAAATTCATGAGTGGAGCTTCTGCTGATTTCAACTCAG 877
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16221 AGGTAGTTATTTTTCAGGAGTGTGATCAGCTGCAGACCTAAAGCTAG 16176
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-09-949-016-12741/c
; Sequence 12741, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12741
; LENGTH: 110403
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12741

Query Match      3.2%; Score 36; DB 4; Length 110403;
Best Local Similarity 50.4%; Pred. No. 16; Mismatches 110; Indels 2; Gaps 1;
Matches 114; Conservative

QY 652 ATTCAAAGACAACGTCATCTGCTGAACAAGCACATTTGACGCATACAAAACATTCCACC 711
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16406 ATATATATATATACACATATATACACACACACATCTATCTTATTAAATTTCTCCCTCT 16347
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 712 AACAGAGCCTTAAAGGACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 771
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16346 AGAGAACCCCTAATACATATACAAAATTTCTTAACCCAAAAGTGTTTAGTGAAGAA 16287
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 772 ACAAAGAAAGCAGCCCACTGTGACTCTTCTCTCGCGGCTGACATGATGATTTCTCCAG 831
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 16286 ATACAGAGGAATGTTAATGCTACTCT--TTCTGAGGCTGACAAAGACAAGCAAGTA 16229
Qy 832 ACAACTTCAAAATTCATGAGTGGAGCTTCTGCTGATCAATCAACTCAG 877
Db 16228 AGGTAGTTATTTTTCAGGAGTGGATCAGCTGCAGACCTAAGCTAG 16183

RESULT 8

US-09-949-016-11782/c
; Sequence 11782, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11782
; LENGTH: 139936
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(139936)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11782

Query Match 3.2%; Score 36; DB 4; Length 139936;
Best Local Similarity 54.5%; Pred. No. 18;
Matches 72; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
Qy 326 AAGGCCCAACAAAGGCGCAAACTGTCTACTAAGAAATCTGCTGAGGCATCTAAA 385
Db 73881 AAGAGTCAATACCCACTGAAGCCACCATTTCAGCGAGGAGACAAAGAAACCTTCCAA 73822
Qy 386 AAGCTCGCCAAAAGTACTGCCCAAAACAGTACAAAGTCACTCAAGCATTTGGGAGA 445
Db 73821 AAGCAAGGCACTGAAAGTACTGAATCAAAACTTAAAGCACTCACACGAGCAAGGAGAAA 73762
Qy 446 CGTGTCCAGAA 457
Db 73761 CATGTTACAAAA 73750

RESULT 9

US-09-949-016-13280/c
; Sequence 13280, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13280
; LENGTH: 139952
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(139952)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13280

Query Match 3.2%; Score 36; DB 4; Length 139952;
Best Local Similarity 54.5%; Pred. No. 18;
Matches 72; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
Qy 326 AAGGCCCAACAAAGGCGCAAACTGTCTACTAAGAAATCTGCTGAGGCATCTAAA 385
Db 73896 AAGAGTCAATACCCACTGAAGCCACCATTTCAGCGAGGAGACAAAGAAACCTTCCAA 73837
Qy 386 AAGCTCGCCAAAAGTACTGCCCAAAACAGTACAAAGTCACTCAAGCATTTGGGAGA 445
Db 73836 AAGCAAGGCACTGAAAGTACTGAATCAAAACTTAAAGCACTCACACGAGCAAGGAGAAA 73777
Qy 446 CGTGTCCAGAA 457
Db 73776 CATGTTACAAAA 73765

RESULT 10

US-09-620-312D-1058
; Sequence 1058, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 1058
; LENGTH: 1450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (397)..(1176)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1450)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-1058


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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53338
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-53338

Query Match          3.1%; Score 35.6; DB 4; Length 601;
Best Local Similarity 53.8%; Pred. No. 0.95;
Matches 71; Conservative 1; Mismatches 60; Indels 0; Gaps 0;

Qy 326 AAAGGCCAAACAACAAGGCCAAACCTGTCTACTAAGAAATCTGCTGCTGAGGCATCTAAA 385
Db 192 AAGAGTCAATACCCTCTGAAGCCACCATTTCACGCGAGGAGACAACAAGAACCCCTCCAC 251
Qy 386 AAGCTCGCCMAAAGCTACTGCCACAAAACGATACACGCTCACTCAAGCATTTTGGGAGA 445
Db 252 AAGCAAGGCCTGAAAGTACTGAATCAAAACTTAAAGCACTCACACGAGSAAAGGGAAAA 311
Qy 446 CGTGGTCCAGAA 457
Db 312 CATGGTACAAAA 323

RESULT 13
US-09-949-016-102602
; Sequence 102602, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102602
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-102602

Query Match          3.1%; Score 34.8; DB 4; Length 601;
Best Local Similarity 53.7%; Pred. No. 1.7;
Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 653 TTCAAAGACAACGGTCATCTGCTGAACAAGCACATTGACGCATACAAAACATTCGCCACA 712
Db 153 TTAAGACGAGAAATGATTAAGCTGAGAGAACATTAAGTAAAGTAAAAAACAGGCTATTTA 212
Qy 713 ACAGAGCCTAAAAAGGACAAAAGAAAAGAAAGCTGATGAAGCTCAGCCCTTTCCCGCAGAGA 772
Db 213 AAAATACAAAAGGAGACAAAAGAAAAGAAATAAATAAGTAAATGACGCATGCCTACTAGA 272
Qy 773 CAAAAGAGCAGCC 786
Db 273 TATAGAAAACAGCC 286

RESULT 14
US-09-949-016-102714
; Sequence 102714, Application US/09949016
; Patent No. 6812339

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102714
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-102714

Query Match          3.1%; Score 34.8; DB 4; Length 601;
Best Local Similarity 53.7%; Pred. No. 1.7;
Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 653 TTCAAGACACAGTCATCTGCTGACACGACATTCGCGCATACACAAACATTCCTCCACCA 712
Db 153 TTAAAGCAGCAAGTAATGATGAAGCTGAAGAAACAATTAGTAAGCTTAAACACAGGCTATTTTA 212

Qy 713 ACAGAGCCTTAAAGACACAAAGAAAAAGACTGTGAGCTCAGCCTTTGCGCGCAGAGA 772
Db 213 AAATACACAAAGGAGACAAAGAAAAAGATTAATAGATGACGATGCGCTACTAGA 272

Qy 773 CAAAAGAACGAGCC 786
Db 273 TATAGAAAAACGCC 286

RESULT 15
US-08-931-999-4
; Sequence 4, Application US/08931999
; Patent No. 6043219
; GENERAL INFORMATION:
; APPLICANT: Iandolo, John J.
; APPLICANT: Crupper, Scott S.
; TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,999
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/710,561
; FILING DATE: 19-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25043-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6755 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus aureus
; STRAIN: UT0007
US-08-931-999-4

Query Match          3.1%; Score 34.8; DB 3; Length 6755;
Best Local Similarity 55.9%; Pred. No. 7.2;
Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Db 6508 AACAGCACAAACAAGCGAACACACACACCAACCAACCAACCAACCAACCAACCAACCAAC 6567

Qy 737 AAAAAGACTGTATGAAGCTCAGCCTTTGCGCGCAGACACAAAGAACAGCAGCCACTGTGA 794
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Job time : 253.39 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2005, 12:53:36 ; Search time 838.5 Seconds
(without alignments)
8291.679 Million cell updates/sec

Title: US-10-764-075-1
Perfect score: 1136
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5662332 seqs, 3060109652 residues

Total number of hits satisfying chosen parameters: 11324664

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

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- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
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- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1136	100.0	1136	US-10-764-075-1	Sequence 1, Appli
2	1136	100.0	1620	US-10-699-936-16	Sequence 16, Appl
3	1136	100.0	24774	US-10-889-447-3	Sequence 3, Appli
4	1136	100.0	28920	US-10-889-447-5	Sequence 5, Appli
5	1136	100.0	28920	US-10-889-447-6	Sequence 6, Appli
6	1136	100.0	29727	US-10-839-729-15	Sequence 15, Appl
7	1136	100.0	29727	US-10-827-757-1	Sequence 1, Appli
8	1136	100.0	29727	US-10-889-447-8	Sequence 8, Appli
9	1136	100.0	29727	US-10-699-936-1	Sequence 1, Appli
10	1136	100.0	29736	US-10-839-729-17	Sequence 17, Appl
11	1136	100.0	29736	US-10-889-447-9	Sequence 9, Appli

12	1136	100.0	29736	19	US-10-699-936-3	Sequence 3, Appli
13	1136	100.0	29742	18	US-10-839-729-16	Sequence 16, Appl
14	1136	100.0	29742	19	US-10-808-187-15	Sequence 15, Appl
15	1136	100.0	29742	19	US-10-808-187-16	Sequence 16, Appl
16	1136	100.0	29742	19	US-10-808-187-240	Sequence 240, Appl
17	1136	100.0	29742	19	US-10-808-187-737	Sequence 737, Appl
18	1136	100.0	29742	19	US-10-808-187-1108	Sequence 1108, Ap
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20	1136	100.0	29742	19	US-10-808-187-1965	Sequence 1965, Ap
21	1136	100.0	29742	19	US-10-889-447-10	Sequence 10, Appl
22	1136	100.0	29751	18	US-10-839-729-14	Sequence 14, Appl
23	1136	100.0	29751	19	US-10-856-529-1	Sequence 1, Appli
24	1136	100.0	29751	19	US-10-626-879-67	Sequence 67, Appl
25	1136	100.0	29751	19	US-10-889-447-1	Sequence 1, Appli
26	1136	100.0	29751	19	US-10-889-447-2	Sequence 2, Appli
27	1136	100.0	29751	19	US-10-699-936-2	Sequence 2, Appli
28	1134.4	99.9	29430	19	US-10-889-447-7	Sequence 7, Appli
29	1131.2	99.6	2304	19	US-10-699-936-7	Sequence 7, Appli
30	1131.2	99.6	2304	19	US-10-699-936-11	Sequence 11, Appl
31	1124	98.9	29291	19	US-10-889-447-4	Sequence 4, Appli
32	41.8	3.7	7359	15	US-10-311-455-1836	Sequence 1836, Ap
33	40.2	3.5	2543	18	US-10-363-345A-30203	Sequence 30203, A
34	40.2	3.5	2543	18	US-10-363-345A-30204	Sequence 30204, A
35	40.2	3.5	2543	19	US-10-363-483A-30203	Sequence 30203, A
36	40.2	3.5	2543	19	US-10-363-483A-30204	Sequence 30204, A
37	39.2	3.5	9830	17	US-10-221-613-112	Sequence 112, App
38	39	3.4	481	18	US-10-357-930-57047	Sequence 57047, A
39	39	3.4	5284	18	US-10-723-860-7691	Sequence 7691, Ap
40	38.8	3.4	852	18	US-10-425-115-19938	Sequence 19938, A
41	38.2	3.4	2544	18	US-10-437-963-74109	Sequence 74109, A
42	38.2	3.4	6888	18	US-10-602-494-252	Sequence 252, App
43	38	3.3	8305	15	US-10-311-455-1541	Sequence 1541, Ap
44	37.8	3.3	2748	19	US-10-741-849-6128	Sequence 6128, Ap
45	37.6	3.3	438	18	US-10-437-963-89737	Sequence 89737, A

ALIGNMENTS

RESULT 1

US-10-764-075-1
; Sequence 1, Application US/10764075
; Publication No. US20040265796A1
; GENERAL INFORMATION:
; APPLICANT: Briese, Thomas
; APPLICANT: Lipkin, Ian W.
; APPLICANT: Palacios, Gustavo
; APPLICANT: Jabado, Omar
; TITLE OF INVENTION: Methods and Kits for Detecting SARS-Associated Coronavirus
; FILE REFERENCE: 5199-87
; CURRENT APPLICATION NUMBER: US/10/764,075
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: Provisional Application 60/463,704
; PRIOR FILING DATE: 2003-04-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1136
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic nucleic acid sequence that includes the 3' non-coding o
; OTHER INFORMATION: region of the SARS-associated coronavirus genome and a portion o
; OTHER INFORMATION: the N gene of the SARS-associated coronavirus genome
US-10-764-075-1

Query Match 100.0%; Score 1136; DB 18; Length 1136;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGCATCGTATGGTTGGCACTGAGGAGCCCTTGATACCCCAAGACCACTTGGCAC 60
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Db 1 AGGCATCGTATGGTTGGCACTGAGGAGCCCTTGATACCCCAAGACCACTTGGCAC 60

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RESULT 2
US-10-699-936-16
; Sequence 16, Application US/10699936
; Publication No. US2005009582A1
; GENERAL INFORMATION:
; APPLICANT: Gillim-Ross, Laura
; APPLICANT: Taylor, Jill
; APPLICANT: Scholl, David R.
; APPLICANT: Wentworth, David E.
; APPLICANT: Jollick, Joseph D.
; TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
; TITLE OF INVENTION: Syndrome Coronavirus
; FILE REFERENCE: DHI-07986
; CURRENT APPLICATION NUMBER: US/10/699,936
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: SARS-CoV ZJ-HZ01
US-10-699-936-16

Query Match 100.0%; Score 1136; DB 19; Length 1620;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 AAAAGGCTTCTACGACAGAGGAAGCAGAGGCGGAGTCAAGCTCTTCTCGCTCTCTCATC 180
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QY 181 ACGTAGTCGCGGTAAATCAAGAAATTTCAACTCTTGGGAGCAGTAGGGGAAATTTCTCTGC 240
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RESULT 3

US-10-889-447-3
 ; Sequence 3, Application US/10889447
 ; Publication No. US20050075307A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Jain, Ravi
 ; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
 ; FILE REFERENCE: RTS-0685US
 ; CURRENT APPLICATION NUMBER: US/10/889,447
 ; CURRENT FILING DATE: 2004-07-12
 ; PRIOR FILING DATE: 2003-07-12
 ; NUMBER OF SEQ ID NOS: 241
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 24774
 ; TYPE: DNA
 ; ORGANISM: SARS coronavirus isolate BJ01
 ; NAME/KEY: misc_feature
 ; LOCATION:
 ; OTHER INFORMATION: n is any nucleotide
 US-10-889-447-3

Query Match 100.0%; Score 1136; DB 19; Length 24774;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 23679 CGCAATCTTAATACAACTGCGCAGGAGCCTTTGAATACACCCAAAGACCCACATTGGCAC 23738
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 23739 AAAAGGCTTCTACGAGAGGAGGAGGAGCGGCGAGTCAAGCCCTCTCTCGCTCCCTCATC 23798

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 241 TCGAATGGCTAGCGGAGGTGGTGAACCTGCGGCTATTTGCTGCTAGACAGATTGAA 300
 23859 TCGAATGGCTAGCGGAGGTGGTGAACCTGCGGCTATTTGCTGCTAGACAGATTGAA 23918
 301 CCAAGCTTGAGACAAAGTTTCTGTTAAAGGCCAAACAAACAAGGCCCAAACTGTCACTAA 360
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 24039 CCAAGCTCACTCAAGCAATTTGGGAGAGCTGGTGCAGAACCAACCAAGGAAATTTTCGGGA 24098
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 24219 AACATGGCTGACTTATCATGGAGCCATTAATTTGGATGACAAAGATTCACAAATTTCAAAGA 24278
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 781 GCAGCCCACTGTGACT 840
 24399 GCAGCCCACTGTGACT 24458
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 901 ACAAGGAGATGGGCTATGTAAGCTTTTCCGCAATTTCCGTTTACGATACATAGTCTACTC 960
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 961 TTGTGCGAATGAATTTCTGTAACCAAGCAAGTAGGTTTGTAGTTAACTTTAATCTC 1020
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 1021 ACATAGCAATCTTAAATCAATGTGTAACTTAGGAGGAGCTTGAAGAGCCACCAATTT 1080
 24639 ACATAGCAATCTTAAATCAATGTGTAACTTAGGAGGAGCTTGAAGAGCCACCAATTT 24698
 1081 TCATCGAGGCCACGCGGAGTACGATCGAGGCTACAGTGAATTAATGCTTAGGGAGGC 1136
 24699 TCATCGAGGCCACGCGGAGTACGATCGAGGCTACAGTGAATTAATGCTTAGGGAGGC 24754

RESULT 4

US-10-889-447-5
 ; Sequence 5, Application US/10889447
 ; Publication No. US20050075307A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Jain, Ravi
 ; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION

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; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 28920
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate BJ03
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-5

Query Match      100.0%; Score 1136; DB 19; Length 28920;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGGCATCGTATGCGGTTGCAACTGAGGAGCGCTTGAATACACCCAAAGACCACATTGGCAC 60
DB      1 AGGCATCGTATGCGGTTGCAACTGAGGAGCGCTTGAATACACCCAAAGACCACATTGGCAC 27827

QY      61 CCGCAATCCTAATAACAATGCTGCCACCGTGTCTACAACCTTCTCAAGNACACATTGCC 120
DB      61 CCGCAATCCTAATAACAATGCTGCCACCGTGTCTACAACCTTCTCAAGNACACATTGCC 27828

QY      121 AAAAGCCTTCTACGAGAGGGAAGCAGAGCGGCGAGTCAAGCCTCTTCTCGCTCTCATC 180
DB      121 AAAAGCCTTCTACGAGAGGGAAGCAGAGCGGCGAGTCAAGCCTCTTCTCGCTCTCATC 27889

QY      181 ACGTAGTCGCGGTAAATTCAGAAATTCAACTCTGCGCAGCAGTAGGGGAAATTCCTCTGC 240
DB      181 ACGTAGTCGCGGTAAATTCAGAAATTCAACTCTGCGCAGCAGTAGGGGAAATTCCTCTGC 27947

QY      241 TCGAATGGCTACGGAGGTGGTGAACCTGCCCTCGGGCTATTGCTGCTAGACAGATTGAA 300
DB      241 TCGAATGGCTACGGAGGTGGTGAACCTGCCCTCGGGCTATTGCTGCTAGACAGATTGAA 28067

QY      301 CCAGCTTGAGAGCAAAAGTTTCTGTTAAAGGCCAAACAAAGGCCAAACTGTCACTAA 360
DB      301 CCAGCTTGAGAGCAAAAGTTTCTGTTAAAGGCCAAACAAAGGCCAAACTGTCACTAA 28068

QY      361 GAAATCTGCTGTGAGGCATCTAAAAAGCCTCGCCAAAACCGTACTGCCACAAAACAGTA 420
DB      361 GAAATCTGCTGTGAGGCATCTAAAAAGCCTCGCCAAAACCGTACTGCCACAAAACAGTA 28127

QY      421 CAACGTCACCTCAAGCATTTGGGAGACGTGTCAGNACAAACCCCAAGGAAATTCGGGA 480
DB      421 CAACGTCACCTCAAGCATTTGGGAGACGTGTCAGNACAAACCCCAAGGAAATTCGGGA 28188

QY      481 CCAAGACCTAATCAGCAAGGAACCTGATTACAAAACATTGGCCGCAAAATTCGCAATTTGC 540
DB      481 CCAAGACCTAATCAGCAAGGAACCTGATTACAAAACATTGGCCGCAAAATTCGCAATTTGC 28247

QY      541 TCCAAGTGCCTCTGCAATCTTTTGGAAATGTACGCAATTCGCAATTCGCAATTCGGG 600
DB      541 TCCAAGTGCCTCTGCAATCTTTTGGAAATGTACGCAATTCGCAATTCGCAATTCGGG 28307

QY      601 ACATGGCTGACTTATCATGGAGCCATTAAATTTGGATGACAAAGATCCCAATTCAGAA 660
DB      601 ACATGGCTGACTTATCATGGAGCCATTAAATTTGGATGACAAAGATCCCAATTCAGAA 28367

QY      661 CAACGTCATCTGCTGAAACAGCACATTGACGCATACAAAACATTCCCAACCAACAGAGCC 720
DB      661 CAACGTCATCTGCTGAAACAGCACATTGACGCATACAAAACATTCCCAACCAACAGAGCC 28427

QY      721 TAAAAAGGCAAAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCGCAGACAGACAAAAGAA 780
DB      721 TAAAAAGGCAAAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCGCAGACAGACAAAAGAA 28487

QY      781 GCAGCCCACTGTGACTCTTCTTCTCGGCTGACATGATGATGATTTCTCCAGACAACTTCA 840
DB      781 GCAGCCCACTGTGACTCTTCTTCTCGGCTGACATGATGATGATTTCTCCAGACAACTTCA 28547

QY      841 AAAATTCCATGATGGAGCTTCTGCTGATTAACCTCAGGCATAAAACATCTCATGATGACCA 900
DB      841 AAAATTCCATGATGGAGCTTCTGCTGATTAACCTCAGGCATAAAACATCTCATGATGACCA 28607

QY      901 ACAAGGAGATGGGCTATGTAACGTTTCCGCAATTCGGTTTACGATACATAGTCTACTC 960
DB      901 ACAAGGAGATGGGCTATGTAACGTTTCCGCAATTCGGTTTACGATACATAGTCTACTC 28667

QY      961 TTGTGCAGATGAATTTCTCGTAACCTAAACAGACACAAGTAGGTTTAACTTTAATCTC 1020
DB      961 TTGTGCAGATGAATTTCTCGTAACCTAAACAGACACAAGTAGGTTTAACTTTAATCTC 28727

QY      1021 ACATAGCAATCTTTAATCAATGTGTAAACATTAGGGAGACTTGAAGAGCCACCACTTT 1080
DB      1021 ACATAGCAATCTTTAATCAATGTGTAAACATTAGGGAGACTTGAAGAGCCACCACTTT 28787

QY      1081 TCATCGAGGCCACCGGAGTAGGATCGAGGTACAGTGAATAATGCTAGGGAGAGC 1136
DB      1081 TCATCGAGGCCACCGGAGTAGGATCGAGGTACAGTGAATAATGCTAGGGAGAGC 28847

QY      1136 TCATCGAGGCCACCGGAGTAGGATCGAGGTACAGTGAATAATGCTAGGGAGAGC 1136
DB      1136 TCATCGAGGCCACCGGAGTAGGATCGAGGTACAGTGAATAATGCTAGGGAGAGC 28903

RESULT 5
US-10-889-447-6
; Sequence 6, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 28920
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate BJ04
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-6

Query Match      100.0%; Score 1136; DB 19; Length 28920;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGGCATCGTATGCGGTTGCAACTGAGGAGCGCTTGAATACACCCAAAGACCACATTGGCAC 60
DB      1 AGGCATCGTATGCGGTTGCAACTGAGGAGCGCTTGAATACACCCAAAGACCACATTGGCAC 27827

QY      61 CCGCAATCCTAATAACAATGCTGCCACCGTGTCTACAACCTTCTCAAGNACAACTTGC 120
DB      61 CCGCAATCCTAATAACAATGCTGCCACCGTGTCTACAACCTTCTCAAGNACAACTTGC 27828

QY      121 AAAAGCCTTCTACGAGAGGGAAGCAGAGCGGCGAGTCAAGCCTCTTCTCGCTCTCATC 180
DB      121 AAAAGCCTTCTACGAGAGGGAAGCAGAGCGGCGAGTCAAGCCTCTTCTCGCTCTCATC 27889

QY      181 ACGTAGTCGCGGTAAATTCAGAAATTCAACTCTGCGCAGCAGTAGGGGAAATTCCTCTGC 240
DB      181 ACGTAGTCGCGGTAAATTCAGAAATTCAACTCTGCGCAGCAGTAGGGGAAATTCCTCTGC 27947

QY      241 TCGAATGGCTACGGAGGTGGTGAACCTGCCCTCGGGCTATTGCTGCTAGACAGATTGAA 300
DB      241 TCGAATGGCTACGGAGGTGGTGAACCTGCCCTCGGGCTATTGCTGCTAGACAGATTGAA 28067

QY      301 CCAGCTTGAGAGCAAAAGTTTCTGTTAAAGGCCAAACAAAGGCCAAACTGTCACTAA 360
DB      301 CCAGCTTGAGAGCAAAAGTTTCTGTTAAAGGCCAAACAAAGGCCAAACTGTCACTAA 28068

QY      361 GAAATCTGCTGTGAGGCATCTAAAAAGCCTCGCCAAAACCGTACTGCCACAAAACAGTA 420
DB      361 GAAATCTGCTGTGAGGCATCTAAAAAGCCTCGCCAAAACCGTACTGCCACAAAACAGTA 28127

QY      421 CAACGTCACCTCAAGCATTTGGGAGACGTGTCAGNACAAACCCCAAGGAAATTCGGGA 480
DB      421 CAACGTCACCTCAAGCATTTGGGAGACGTGTCAGNACAAACCCCAAGGAAATTCGGGA 28188

QY      481 CCAAGACCTAATCAGCAAGGAACCTGATTACAAAACATTGGCCGCAAAATTCGCAATTTGC 540
DB      481 CCAAGACCTAATCAGCAAGGAACCTGATTACAAAACATTGGCCGCAAAATTCGCAATTTGC 28247

QY      541 TCCAAGTGCCTCTGCAATCTTTTGGAAATGTACGCAATTCGCAATTCGCAATTCGGG 600
DB      541 TCCAAGTGCCTCTGCAATCTTTTGGAAATGTACGCAATTCGCAATTCGCAATTCGGG 28307

QY      601 ACATGGCTGACTTATCATGGAGCCATTAAATTTGGATGACAAAGATCCCAATTCAGAA 660
DB      601 ACATGGCTGACTTATCATGGAGCCATTAAATTTGGATGACAAAGATCCCAATTCAGAA 28367

QY      661 CAACGTCATCTGCTGAAACAGCACATTGACGCATACAAAACATTCCCAACCAACAGAGCC 720
DB      661 CAACGTCATCTGCTGAAACAGCACATTGACGCATACAAAACATTCCCAACCAACAGAGCC 28427

QY      721 TAAAAAGGCAAAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCGCAGACAGACAAAAGAA 780
DB      721 TAAAAAGGCAAAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCGCAGACAGACAAAAGAA 28487

QY      781 GCAGCCCACTGTGACTCTTCTTCTCGGCTGACATGATGATGATTTCTCCAGACAACTTCA 840
DB      781 GCAGCCCACTGTGACTCTTCTTCTCGGCTGACATGATGATGATTTCTCCAGACAACTTCA 28547
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Qy 301 CCAGCTTGAGGCAAGTTTCTGGTAAAGCCCAACAAACAAGGCGCAAACTGTCACTAA 360
Db 28068 CCAGCTTGAGGCAAGTTTCTGGTAAAGCCCAACAAACAAGGCGCAAACTGTCACTAA 28127
Qy 361 GAAATCTGCTGAGGCAATCTAAAGCTCTGCGCCCAAAAGCTGCTGCAAAAACAGTA 420
Db 28128 GAAATCTGCTGAGGCAATCTAAAGCTCTGCGCCCAAAAGCTGCTGCAAAAACAGTA 28187
Qy 421 CAACGTCACCTCAAGCAATTTGGGAGAGCTGTGAGCAAGCAAAACCAAGGAAATTTGGGGG 480
Db 28188 CAACGTCACCTCAAGCAATTTGGGAGAGCTGTGAGCAAGCAAAACCAAGGAAATTTGGGGG 28247
Qy 481 CCAAGCACTTAATCAGACAAAGAACTGATTACAAACATTTGGCCGCAAAATTTGC 540
Db 28248 CCAAGCACTTAATCAGACAAAGAACTGATTACAAACATTTGGCCGCAAAATTTGC 28307
Qy 541 TCCAAGTGCTCTGCAATCTTTGGAATGTCAACCATTTGGCATGGAATGCAATTTGGG 600
Db 28308 TCCAAGTGCTCTGCAATCTTTGGAATGTCAACCATTTGGCATGGAATGCAATTTGGG 28367
Qy 601 AACATGGCTGACTTATCATGAGCCATTAAATTTGGATGACAAAGATCCAAATTTCAAAGA 660
Db 28368 AACATGGCTGACTTATCATGAGCCATTAAATTTGGATGACAAAGATCCAAATTTCAAAGA 28427
Qy 661 CAACGTCATCTGCTGAACAAAGCAATTTGACGCAATACAAACATTTCCCAACACAGAGCC 720
Db 28428 CAACGTCATCTGCTGAACAAAGCAATTTGACGCAATACAAACATTTCCCAACACAGAGCC 28487
Qy 721 TAAAAAGGCAAAAAGAAAAGACTGATGAGCTCAGCCCTTTCCGCGAGAGACAAAAGAA 780
Db 28488 TAAAAAGGCAAAAAGAAAAGACTGATGAGCTCAGCCCTTTCCGCGAGAGACAAAAGAA 28547
Qy 781 GCAGCCCACTGTCACTCTCTCTCGCGCTGACATGGATGATTTCTCCAGACAACTTCA 840
Db 28548 GCAGCCCACTGTCACTCTCTCTCGCGCTGACATGGATGATTTCTCCAGACAACTTCA 28607
Qy 841 AAATTCATGAGTGGAGCTTCTGCTGATTAACCTCAGGCAATAAACACTCATGATGACCAC 900
Db 28608 AAATTCATGAGTGGAGCTTCTGCTGATTAACCTCAGGCAATAAACACTCATGATGACCAC 28667
Qy 901 ACAGGCAAGTGGCTATGTAACGTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 960
Db 28668 ACAGGCAAGTGGCTATGTAACGTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 28727
Qy 961 TTGTGCAGAAATGAATTTCTCTGTAACAAAGCAAGCAAGTAGTGTGTTAGTTAACTTAACTC 1020
Db 28728 TTGTGCAGAAATGAATTTCTCTGTAACAAAGCAAGCAAGTAGTGTGTTAGTTAACTTAACTC 28787
Qy 1021 ACATAGCAATCTTTTAATGTTGTAACATTTAGGAGGAGCTTGAAGAGCCACCACTTT 1080
Db 28788 ACATAGCAATCTTTTAATGTTGTAACATTTAGGAGGAGCTTGAAGAGCCACCACTTT 28847
Qy 1081 TCATCAGGCGCCGCGAGTACATCGAGGTCAGTGAATGCTAGGAGAGC 1136
Db 28848 TCATCAGGCGCCGCGAGTACATCGAGGTCAGTGAATGCTAGGAGAGC 28903
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RESULT 6

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US-10-839-729-15
; Sequence 15, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 15
; LENGTH: 29727
; TYPE: DNA
; ORGANISM: SARS Coronavirus
; US-10-839-729-15
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Query Match 100.0%; Score 1136; DB 18; Length 29727;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AGGCATCGTATGGTTGCAACTCAGGGAGCCTTGAATACACCCCAAGACCCACATTGGCAC 60
Db 28506 AGGCATCGTATGGTTGCAACTCAGGGAGCCTTGAATACACCCCAAGACCCACATTGGCAC 28565
Qy 61 CGCAATCTCTAATAACAAATGCTGCCACCGTGTACAACTTCTCTCAAGGAAACAACATTGCC 120
Db 28566 CGCAATCTCTAATAACAAATGCTGCCACCGTGTACAACTTCTCTCAAGGAAACAACATTGCC 28625
Qy 121 AAAGGCTTCTACGACAGAGGAAAGACAGAGCGGAGCTCAAGCCTCTTCTCGCTCCTCATC 180
Db 28626 AAAGGCTTCTACGACAGAGGAAAGACAGAGCGGAGCTCAAGCCTCTTCTCGCTCCTCATC 28685
Qy 181 AGTAGTCGCGTAAATTTCAAGAAATTTCACTCTCGCGCAGTGTAGGGAAATTTCTCCTGC 240
Db 28686 AGTAGTCGCGTAAATTTCAAGAAATTTCACTCTCGCGCAGTGTAGGGAAATTTCTCCTGC 28745
Qy 241 TCGAATGGCTAGCGGAGGTGGTGAATCTGCCCTCGCGCTATTGCTGTAGACAGATTGAA 300
Db 28746 TCGAATGGCTAGCGGAGGTGGTGAATCTGCCCTCGCGCTATTGCTGTAGACAGATTGAA 28805
Qy 301 CCAGCTTGAGAGCAAAAGTTTCTGGTAAAGCCCAACAAACAAGGCGCAAACTGTCACTAA 360
Db 28806 CCAGCTTGAGAGCAAAAGTTTCTGGTAAAGGCCAAACAACAAGGCGCAAACTGTCACTAA 28865
Qy 361 GAAATCTGCTGAGGCACTTAAAGAGCCTCGCCAAAGACGTAAGTCTGCCCAACAAACAGTA 420
Db 28866 GAAATCTGCTGAGGCACTTAAAGAGCCTCGCCAAAGACGTAAGTCTGCCCAACAAACAGTA 28925
Qy 421 CAAAGCTCACTCAAGCAATTTGGGAGAGCTGTGTCAGAAACAAACCAAGGAAATTTCCGGGA 480
Db 28926 CAAAGCTCACTCAAGCAATTTGGGAGAGCTGTGTCAGAAACAAACCAAGGAAATTTCCGGGA 28985
Qy 481 CCAAGCACTTAATCAGACAAAGGAACTGATTACAAACATTTGGCCGCAAAATTTGC 540
Db 28986 CCAAGCACTTAATCAGACAAAGGAACTGATTACAAACATTTGGCCGCAAAATTTGC 29045
Qy 541 TCCNAGTGCTCTGCAATTTCTTGGATGTGCGCATTTGCGATGCGAGTCAACCTTCGGG 600
Db 29046 TCCNAGTGCTCTGCAATTTCTTGGATGTGCGCATTTGCGATGCGAGTCAACCTTCGGG 29105
Qy 601 AACATGGCTGACTTATCATGAGGCCATTAAATTTGGATGACAAAGATCCCAATTTCAAAGA 660
Db 29106 AACATGGCTGACTTATCATGAGGCCATTAAATTTGGATGACAAAGATCCCAATTTCAAAGA 29165
Qy 661 CAAAGCTCACTGTGTAACAAAGCAATTCAGCGATACAAAAACATTTCCCAACCAAGAGCC 720
Db 29166 CAAAGCTCACTGTGTAACAAAGCAATTCAGCGATACAAAAACATTTCCCAACCAAGAGCC 29225
Qy 721 TAAAAAGGCAAAAAGAAAAGACTGATGAGCTCAGCCCTTTCCGCGAGAGACAAAAGAA 780
Db 29226 TAAAAAGGCAAAAAGAAAAGACTGATGAGCTCAGCCCTTTCCGCGAGAGACAAAAGAA 29285
Qy 781 GCAGCCCACTGTGACTCTTCTTCTCGCGCTGACATGGATGATTTCTCCAGACAACTTCA 840
Db 29286 GCAGCCCACTGTGACTCTTCTTCTCGCGCTGACATGGATGATTTCTCCAGACAACTTCA 29345
Qy 841 AAATTCATGAGTGGAGCTTCTGCTGATTAACACTCAGGCAATAAACACTCATGATGACCAC 900
Db 29346 AAATTCATGAGTGGAGCTTCTGCTGATTAACACTCAGGCAATAAACACTCATGATGACCAC 29405
Qy 901 ACAAGGCAAGTGGCTATGTAACGTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 960
Db 29406 ACAAGGCAAGTGGCTATGTAACGTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 29465
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QY 61 CCGCAATCTTAATAACAATCTGCTCCACCGGTGTACTAACTTCTCAAGGAACAACATTGCC 120
Db 28566 CCGCAATCTTAATAACAATCTGCTCCACCGGTGTACTAACTTCTCAAGGAACAACATTGCC 28625
QY 121 AAAAGGCTTCTACGACAGGGGAAGCAGAGGGGCGAGTCAAGCTCTTCTCGCTCCTCATC 180
Db 28626 AAAAGGCTTCTACGACAGGGGAAGCAGAGGGGCGAGTCAAGCTCTTCTCGCTCCTCATC 28685
QY 181 ACCTAGTCGGGTAAATTAAGAAATTCAACTCTCTGGCAGCAGTAGGGGAATTTCTCTGTC 240
Db 28686 ACCTAGTCGGGTAAATTAAGAAATTCAACTCTCTGGCAGCAGTAGGGGAATTTCTCTGTC 28745
QY 241 TCGAATGGCTAGCGGAGGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTGAA 300
Db 28746 TCGAATGGCTAGCGGAGGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTGAA 28805
QY 301 CCAGCTTGAGAGCAAAAGTTTCTGTAAGGCCAACACACAGAGGCCCAACTCTCACTAA 360
Db 28806 CCAGCTTGAGAGCAAAAGTTTCTGTAAGGCCAACACACAGAGGCCCAACTCTCACTAA 28865
QY 361 GAAATCTGCTGTGAGGCATCTAAAAAGCCTCGCCAAAACGTAAGTCCCAACAAAACAGTA 420
Db 28866 GAAATCTGCTGTGAGGCATCTAAAAAGCCTCGCCAAAACGTAAGTCCCAACAAAACAGTA 28925
QY 421 CAAAGCTTAATCAGACAGGAGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTG 480
Db 28926 CAAAGCTTAATCAGACAGGAGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTG 28985
QY 481 CCAAGCTTAATCAGACAGGAGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTG 540
Db 28986 CCAAGCTTAATCAGACAGGAGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTG 29045
QY 541 TCCAAGTGGCTCTGCAATCTTTTGGAAATGTCAAGCATTTGGCATGGAAAGTCAACCTTCGGG 600
Db 29046 TCCAAGTGGCTCTGCAATCTTTTGGAAATGTCAAGCATTTGGCATGGAAAGTCAACCTTCGGG 29105
QY 601 AACATGGCTGACTTATATGAGGCCATTTAAATTTGGATGACAAAGATCCCAATTCAGAA 660
Db 29106 AACATGGCTGACTTATATGAGGCCATTTAAATTTGGATGACAAAGATCCCAATTCAGAA 29165
QY 661 CAAAGCTTAATCAGACAGGAGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTG 720
Db 29166 CAAAGCTTAATCAGACAGGAGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTG 29225
QY 721 TAAAAAGGCAAAAAGAAAGACTGATGAAGCTCAGCCCTTTGCGCAGAGACAAAAGAA 780
Db 29226 TAAAAAGGCAAAAAGAAAGACTGATGAAGCTCAGCCCTTTGCGCAGAGACAAAAGAA 29285
QY 781 GCAGCCCACTGTGACTCTTCTCTCGGCTGACATGGATGATTTCTCCAGACAACTTCA 840
Db 29286 GCAGCCCACTGTGACTCTTCTCTCGGCTGACATGGATGATTTCTCCAGACAACTTCA 29345
QY 841 AAATTCATGAGTGGAGTCTCTGATTCMACTCAGGCATTAACACTCATGATGACCCAC 900
Db 29346 AAATTCATGAGTGGAGTCTCTGATTCMACTCAGGCATTAACACTCATGATGACCCAC 29405
QY 901 ACAAGCAGATGGCTATGTAACGTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 960
Db 29406 ACAAGCAGATGGCTATGTAACGTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 29465
QY 961 TTGTGAGAGTAATTTCTCGTAACTAAACAGCACAAGTAGTGGTTTGTAACTTAACTCTC 1020
Db 29466 TTGTGAGAGTAATTTCTCGTAACTAAACAGCACAAGTAGTGGTTTGTAACTTAACTCTC 29525
QY 1021 ACATAGCAATCTTTAATCAATGTGTAACATTAGGAGGACTTCAAGAGGCCACCATTTT 1080
Db 29526 ACATAGCAATCTTTAATCAATGTGTAACATTAGGAGGACTTCAAGAGGCCACCATTTT 29585
QY 1081 TCATCAGGCCACCGCGAGTACCATCGAGGGTACAGTGAATTAATGCTAGGGAGAGC 1136
Db 29586 TCATCAGGCCACCGCGAGTACCATCGAGGGTACAGTGAATTAATGCTAGGGAGAGC 29641
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RESULT 9

US-10-699-936-1
; Sequence 1, Application US/10699936
; Publication No. US20050095582A1
; GENERAL INFORMATION:

; APPLICANT: Gillim-Ross, Laura

; APPLICANT: Taylor, Jill

; APPLICANT: Scholl, David R.

; APPLICANT: Wentworth, David E.

; APPLICANT: Jollick, Joseph D.

; TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory

; TITLE OF INVENTION: Syndrome Coronavirus

; FILE REFERENCE: DHI-07986

; CURRENT APPLICATION NUMBER: US/10/699,936

; CURRENT FILING DATE: 2003-11-03

; NUMBER OF SEQ ID NOS: 87

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 29727

; TYPE: DNA

; ORGANISM: SARS coronavirus Urbani

US-10-699-936-1

Query Match 100.0%; Score 1136; DB 19; Length 29727;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGGCATCGTATGGTTTGCACACTGAGGGAGCCTTGAATACACCCAAAGACCACATTGGCAC 60
Db 28506 AGGCATCGTATGGTTTGCACACTGAGGGAGCCTTGAATACACCCAAAGACCACATTGGCAC 28565
QY 61 CCGCAATCTTAATAACAATGTCTGCCACCGTGTCTAACACTTCTCTCAAGGAACAACATTGCC 120
Db 28566 CCGCAATCTTAATAACAATGTCTGCCACCGTGTCTAACACTTCTCTCAAGGAACAACATTGCC 28625
QY 121 AAAAGCTTCTACGACAGGGGAAGCAGAGCGGCGAGTCAAGCCTCTTCTCGCTCCTCATC 180
Db 28626 AAAAGCTTCTACGACAGGGGAAGCAGAGCGGCGAGTCAAGCCTCTTCTCGCTCCTCATC 28685
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QY 241 TCGAATGGCTAGCGGAGGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTGAA 300
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Db 28806 CCAGCTTGAGAGCAAAAGTTTCTGGTAAAGGCCAACAAACAAGGCCAAACTGTCTACTAA 28865
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Db 28866 GAAATCTGCTGTGAGGCATCTAAAAAGCCTCGCCAAAACGTAAGTCCCAACAAAACAGTA 28925
QY 421 CAAAGCTTAATCAGACAGGAGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTG 480
Db 28926 CAAAGCTTAATCAGACAGGAGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTG 28985
QY 481 CCAAGCTTAATCAGACAGGAGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTG 540
Db 28986 CCAAGCTTAATCAGACAGGAGTGGTGAACCTGCCCTCGCGCTATTGCTGTAGACAGATTG 29045
QY 541 TCCAAGTGGCTCTGCAATCTTTTGGAAATGTCAAGCATTTGGCATGGAAAGTCAACCTTCGGG 600
Db 29046 TCCAAGTGGCTCTGCAATCTTTTGGAAATGTCAAGCATTTGGCATGGAAAGTCAACCTTCGGG 29105
QY 601 AACATGGCTGACTTATATGAGGCCATTTAAATTTGGATGACAAAGATCCCAATTCAGAA 660
Db 29106 AACATGGCTGACTTATATGAGGCCATTTAAATTTGGATGACAAAGATCCCAATTCAGAA 29165
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Db 29166 CAAAGTCTACTGCTGAACAAGCAGCATTTGACGCGTAAACAAATTTCCACCAACAGAGCC 29225
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QY 721 TAAAAAGGACAAAAAGAAAGACTGATGAAGCTTTCAGCCTTTGCGCGCAGAGACAAAAGAA 780
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|
Db 29226 TAAAAAGGACAAAAAGAAAGACTGATGAAGCTTTCAGCCTTTGCGCGCAGAGACAAAAGAA 29285
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|
|
QY 781 CGAGCCCACTGTGACTCTTCTTCTCGCGGCTGACATGGATGATTTCTCCAGACAACTTCA 840
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|
|
Db 29286 CGAGCCCACTGTGACTCTTCTTCTCGCGGCTGACATGGATGATTTCTCCAGACAACTTCA 29345
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QY 841 AAATTCATGAGTGGAGCTTCTGCTGATTAACACTCAGGCATTAACACATCATGATGACCCAC 900
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Db 29346 AAATTCATGAGTGGAGCTTCTGCTGATTAACACTCAGGCATTAACACATCATGATGACCCAC 29405
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|
|
QY 901 ACAAGGCAGATGGGCTATGTAACGTTTTCGCAATTCGTTTACGATACATGCTACTC 960
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|
|
Db 29406 ACAAGGCAGATGGGCTATGTAACGTTTTCGCAATTCGTTTACGATACATGCTACTC 29465
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|
|
QY 961 TTGTGCAGAAATTAATTCGTAACCTAAACAGCAGCAGTAGGTTTAACTTTAACTTCTC 1020
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|
|
Db 29466 TTGTGCAGAAATTAATTCGTAACCTAAACAGCAGCAGTAGGTTTAACTTTAACTTCTC 29525
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|
|
QY 1021 ACATAGCAATCTTTAATCAATGTGTAACATTAAGGAGGACTTTGAAGAGCCACCACTTT 1080
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Db 29526 ACATAGCAATCTTTAATCAATGTGTAACATTAAGGAGGACTTTGAAGAGCCACCACTTT 29585
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QY 1081 TCATGAGGCCACGGGAGTACGATCGAGGGTACAGTGAATATGCTAGGGAGGC 1136
|
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|
Db 29586 TCATGAGGCCACGGGAGTACGATCGAGGGTACAGTGAATATGCTAGGGAGGC 29641
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RESULT 10
US-10-839-729-17
; Sequence 17, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; PRIOR FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 29736
; TYPE: DNA
; ORGANISM: SARS Coronavirus
US-10-839-729-17
Query Match 100.0%; Score 1136; DB 18; Length 29736;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGCATCGTATGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCAATTGGCAC 60
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Db 28491 AGGCATCGTATGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCAATTGGCAC 28550
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QY 61 CGCAGATCTTAATAACAATGTCACACCGTGTCTACAACTTCTCAAGGAACAACATTGCC 120
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|
|
Db 28551 CGCAGATCTTAATAACAATGTCACACCGTGTCTACAACTTCTCAAGGAACAACATTGCC 28610
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QY 121 AAAAGCTTCTTACGCGAGAGGGAAGCAGAGCGGCGAGTCAAGCCTCTTCTCGCTCTCATPC 180
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|
Db 28611 AAAAGCTTCTTACGCGAGAGGGAAGCAGAGCGGCGAGTCAAGCCTCTTCTCGCTCTCATC 28670
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|
QY 181 AGTAGTCGGGTAAATTAAGAAATTAACACTCTGCGCAGCAGTAGGGGAAATTCCTCTGC 240
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|
|
Db 28671 AGTAGTCGGGTAAATTAAGAAATTAACACTCTGCGCAGCAGTAGGGGAAATTCCTCTGC 28730
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QY 241 TCGAATGGCTAGCGGAGGTTGGTGAACCTGCGCTCGCGCTATTGCTGCTAGACAGATTGAA 300
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Db 28731 TCGAATGCTAGCGGAGTGGTGAACCTGCGCTTATGCTGCTAGACAGATTGAA 28790
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QY 301 CCAGTTGAGAGCAAAAGTTTCTGTTAAAGGCCAACAAACAAAGCCAAAACCTGTCTACTAA 360
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|
|
Db 28791 CCAGTTGAGAGCAAAAGTTTCTGTTAAAGGCCAACAAACAAAGCCAAAACCTGTCTACTAA 28850
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QY 361 GAAATCTCTGCTGAGGCTCTAAAAGCCTCGCCAAAACGTCAGTCCACAAAACAGTA 420
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Db 28851 GAAATCTCTGCTGAGGCTCTAAAAGCCTCGCCAAAACGTCAGTCCACAAAACAGTA 28910
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QY 421 CAACTGCTCACTCAAGCATTTGGGAGACGTTGTCAGAACAAAACCCAAAGGAAATTTCCGGGA 480
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|
|
Db 28911 CAACTGCTCACTCAAGCATTTGGGAGACGTTGTCAGAACAAAACCCAAAGGAAATTTCCGGGA 28970
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QY 481 CCAAGACCTAATCAGAACAGGAACCTGATTCAAACTTTGGCGCGGCAAAATGTCACAAATTTGC 540
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Db 28971 CCAAGACCTAATCAGAACAGGAACCTGATTCAAACTTTGGCGCGGCAAAATGTCACAAATTTGC 29030
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QY 541 TCCAGTGCCTCTGCTATTTTGGAACTCTCAGCAATTCGCGATGGAAGTCAACACCTTTCCGG 600
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Db 29031 TCCAGTGCCTCTGCTATTTTGGAACTCTCAGCAATTCGCGATGGAAGTCAACACCTTTCCGG 29090
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QY 601 AACATGGCTGACTTATCATGAGGCCATTTAAATTTGGATCAAAAGATCCCAATTTCAAGA 660
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Db 29091 AACATGGCTGACTTATCATGAGGCCATTTAAATTTGGATCAAAAGATCCCAATTTCAAGA 29150
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QY 661 CAACTGCTACTGCTGAAACAGCAGCATTTGACGCATACAAAACATTTCCACCAACAGAGCC 720
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Db 29151 CAACTGCTACTGCTGAAACAGCAGCATTTGACGCATACAAAACATTTCCACCAACAGAGCC 29210
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QY 721 TAAAGGACACAAAAGAAAAGACTGATGAAGCTCAGCCTTTGCGCGCAGAGACAAAAGAA 780
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Db 29211 TAAAGGACACAAAAGAAAAGACTGATGAAGCTCAGCCTTTGCGCGCAGAGACAAAAGAA 29270
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QY 781 GCAGCCCACTGTGACTCTTCTTCTCGCGCTGACATGGATGATTTCTCCAGACAACTTCA 840
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Db 29271 GCAGCCCACTGTGACTCTTCTTCTCGCGCTGACATGGATGATTTCTCCAGACAACTTCA 29330
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QY 841 AAATTCATGAGTGGAGCTTCTGCTGATTAACACTCAGGCATTAACACATCATGATGACCCAC 900
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Db 29331 AAATTCATGAGTGGAGCTTCTGCTGATTAACACTCAGGCATTAACACATCATGATGACCCAC 29390
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QY 901 ACAAGGCAGATGGGCTATGTAACGTTTTCGCAATTCGTTTACGATACATGCTACTC 960
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|
|
Db 29391 ACAAGGCAGATGGGCTATGTAACGTTTTCGCAATTCGTTTACGATACATGCTACTC 29450
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QY 961 TTGTGCAGAAATTAATTCGTAACCTTAACAGCAGCAGTAGGTTTAACTTTAACTTCTC 1020
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Db 29451 TTGTGCAGAAATTAATTCGTAACCTTAACAGCAGCAGTAGGTTTAACTTTAACTTCTC 29510
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QY 1021 ACATAGCAATCTTTAATCAATGTGTAACCTTAAGGAGGACTTTGAAGAGCCACCACTTT 1080
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Db 29511 ACATAGCAATCTTTAATCAATGTGTAACCTTAAGGAGGACTTTGAAGAGCCACCACTTT 29570
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QY 1081 TCATCGAGGCCACGGGAGTACGATCGAGGGTACAGTGAATATGCTAGGGAGGC 1136
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Db 29571 TCATCGAGGCCACGGGAGTACGATCGAGGGTACAGTGAATATGCTAGGGAGGC 29626
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RESULT 11
US-10-889-447-9
; Sequence 9, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; PRIOR FILING DATE: 2003-07-12
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; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 29736
; TYPE: DNA
; ORGANISM: SARS coronavirus CUHK-W1
US-10-889-447-9

Query Match 100.0%; Score 1136; DB 19; Length 29736;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCATCGTATGGTTCACATGAGGAGGCTTGAATACACCCAAAGACACAAATTGGCAC 60
DB 28491 AGGCATCGTATGGTTCACATGAGGAGGCTTGAATACACCCAAAGACACAAATTGGCAC 28550

QY 61 CCGCAATCCTTAATAACAATCTGCCCGGTGTACAACTTCTCAAGGAACAACTTGCC 120
DB 28551 CCGCAATCCTTAATAACAATCTGCCCGGTGTACAACTTCTCAAGGAACAACTTGCC 28610

QY 121 AAAAGGCTTCTACGCAGAGGAAAGCAGAGCGGCAGTCAAGCCCTCTTCTCGCTCCTCATC 180
DB 28611 AAAAGGCTTCTACGCAGAGGAAAGCAGAGCGGCAGTCAAGCCCTCTTCTCGCTCCTCATC 28670

QY 181 ACGTAGTCGGGTAAATTCAGAAATTCAACTCTCGCAGCAGTATGGGAAATTTCTCTGTC 240
DB 28671 ACGTAGTCGGGTAAATTCAGAAATTCAACTCTCGCAGCAGTATGGGAAATTTCTCTGTC 28730

QY 241 TCGAATGGCTAGCGGAGGTGGTGAAGTGGCTTCTCGCTTCTGCTAGACAGATTGAA 300
DB 28731 TCGAATGGCTAGCGGAGGTGGTGAAGTGGCTTCTCGCTTCTGCTAGACAGATTGAA 28790

QY 301 CCAGCTTGAGAGCAAAAGTTTCTGGTAAAGGCCAAACAAAGGCCAAACTGTCACTAA 360
DB 28791 CCAGCTTGAGAGCAAAAGTTTCTGGTAAAGGCCAAACAAAGGCCAAACTGTCACTAA 28850

QY 361 GAAATCTGCTGTGAGCATCTAAAAGCTCGCCAAAACAGTACTGCCCAAAAACAGTA 420
DB 28851 GAAATCTGCTGTGAGCATCTAAAAGCTCGCCAAAACAGTACTGCCCAAAAACAGTA 28910

QY 421 CACGTCACCTCAAGCAATTTGGGAGAGTGGTGCAGAAACAAACCAAGGAAATTTCCGGGA 480
DB 28911 CACGTCACCTCAAGCAATTTGGGAGAGTGGTGCAGAAACAAACCAAGGAAATTTCCGGGA 28970

QY 481 CCAAGACCTAATCAGACAAAGGAACTGATTAACAACATTTGGCCGCAAAATTCGCAATTTGC 540
DB 28971 CCAAGACCTAATCAGACAAAGGAACTGATTAACAACATTTGGCCGCAAAATTCGCAATTTGC 29030

QY 541 TCCAAGTGCTCTGCAATTTCTTGGAAATGTCAAGCATTTGGCATGGAAGTCAACCTTCGGG 600
DB 29031 TCCAAGTGCTCTGCAATTTCTTGGAAATGTCAAGCATTTGGCATGGAAGTCAACCTTCGGG 29090

QY 601 AACATGGCTGACTTATCATGGAGCCATTAATTTGGATGACAAAGATCCCAATTTCAAAGA 660
DB 29091 AACATGGCTGACTTATCATGGAGCCATTAATTTGGATGACAAAGATCCCAATTTCAAAGA 29150

QY 661 CAACTGCTACTCTGCAAGCAAGCAGTATGACGATCAAAAACATTTCCACCAACAGAGCC 720
DB 29151 CAACTGCTACTCTGCAAGCAAGCAGTATGACGATCAAAAACATTTCCACCAACAGAGCC 29210

QY 721 TAAAAAGGCAAAAAGAAAAGACTGATGAAGCTCAGCCCTTTGGCCGAGAGACAAAGAA 780
DB 29211 TAAAAAGGCAAAAAGAAAAGACTGATGAAGCTCAGCCCTTTGGCCGAGAGACAAAGAA 29270

QY 781 GCAGCCCACTGTGACTTCTTCTCTCGGCTGACATGGATGATTTCTCCAGACAACTTCA 840
DB 29271 GCAGCCCACTGTGACTTCTTCTCTCGGCTGACATGGATGATTTCTCCAGACAACTTCA 29330

QY 841 AAATTCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATGACCA 900
DB 29331 AAATTCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATGACCA 29390

QY 901 ACAAGCAGATGGGCTATGTAAACGTTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 960

DB 29391 ACAAGCAGATGGGCTATGTAAACGTTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 29450

QY 961 TTGTGCAGAAATGAATTTCTCGTAACTAAACAGCAAGTAGTGTAGTTAACTTTAAATCTC 1020

DB 29451 TTGTGCAGAAATGAATTTCTCGTAACTAAACAGCAAGTAGTGTAGTTAACTTTAAATCTC 29510

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DB 29511 ACATAGCAATCTTTTAATCAATGTGTAACTATTAGGAGGACTTGAAGAGAGCCACACATTT 29570

QY 1081 TCATCGAGGCCACCGCGAGTACGATCGAGGGTACAGTGAATAATGCTTAGGGAGAGC 1136

DB 29571 TCATCGAGGCCACCGCGAGTACGATCGAGGGTACAGTGAATAATGCTTAGGGAGAGC 29626

RESULT 12
US-10-699-936-3
; Sequence 3, Application US/10699936
; Publication No. US20050095582A1
; GENERAL INFORMATION:
; APPLICANT: Gillim-Ross, Laura
; APPLICANT: Taylor, Jill
; APPLICANT: Scholl, David R.
; APPLICANT: Wentworth, David E.
; APPLICANT: Jollick, Joseph D.
; TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
; TITLE OF INVENTION: Syndrome Coronavirus
; FILE REFERENCE: DHI-07986
; CURRENT APPLICATION NUMBER: US/10/699, 936
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 29736
; TYPE: DNA
; ORGANISM: SARS coronavirus CUHK-W1
US-10-699-936-3

Query Match 100.0%; Score 1136; DB 19; Length 29736;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCATCGTATGGTTCGCAATCGAGGAGCCTTGAATACACCCAAAGACACAAATTGGCAC 60
DB 28491 AGGCATCGTATGGTTCGCAATCGAGGAGCCTTGAATACACCCAAAGACACAAATTGGCAC 28550

QY 61 CCGCAATCCTTAATAACAATGTGCGCACCGTGTCAAACTTCTCTCAAGGAACAACTTGCC 120
DB 28551 CCGCAATCCTTAATAACAATGTGCGCACCGTGTCAAACTTCTCTCAAGGAACAACTTGCC 28610

QY 121 AAAAGGCTTCTACGCAGAGGAAAGCAGAGCGGCAGTCAAGCCCTCTTCTCGCTCCTCATC 180
DB 28611 AAAAGGCTTCTACGCAGAGGAAAGCAGAGCGGCAGTCAAGCCCTCTTCTCGCTCCTCATC 28670

QY 181 ACGTAGTCGGGTAAATTCAGAAATTCAACTCTCGCAGCAGTATGGGAAATTTCTCTGTC 240
DB 28671 ACGTAGTCGGGTAAATTCAGAAATTCAACTCTCGCAGCAGTATGGGAAATTTCTCTGTC 28730

QY 241 TCGAATGGCTAGCGGAGGTGGTGAAGTGGCTTCTCGCTTCTGCTAGACAGATTGAA 300
DB 28731 TCGAATGGCTAGCGGAGGTGGTGAAGTGGCTTCTCGCTTCTGCTAGACAGATTGAA 28790

QY 301 CCAGCTTGAGAGCAAAAGTTTCTGGTAAAGGCCAAACAAAGGCCAAACTGTCACTAA 360
DB 28791 CCAGCTTGAGAGCAAAAGTTTCTGGTAAAGGCCAAACAAAGGCCAAACTGTCACTAA 28850

QY 361 GAAATCTGCTGTGAGCATCTAAAAGCTCGCCAAAACAGTACTGCCCAAAAACAGTA 420
DB 28851 GAAATCTGCTGTGAGCATCTAAAAGCTCGCCAAAACAGTACTGCCCAAAAACAGTA 28910

QY 421 CACGTCACCTCAAGCAATTTGGGAGAGTGGTGCAGAAACAAACCAAGGAAATTTCCGGGA 480
DB 28911 CACGTCACCTCAAGCAATTTGGGAGAGTGGTGCAGAAACAAACCAAGGAAATTTCCGGGA 28970

QY 481 CCAAGACCTAATCAGACAAAGGAACTGATTAACAACATTTGGCCGCAAAATTCGCAATTTGC 540
DB 28971 CCAAGACCTAATCAGACAAAGGAACTGATTAACAACATTTGGCCGCAAAATTCGCAATTTGC 29030

QY 541 TCCAAGTGCTCTGCAATTTCTTGGAAATGTCAAGCATTTGGCATGGAAGTCAACCTTCGGG 600
DB 29031 TCCAAGTGCTCTGCAATTTCTTGGAAATGTCAAGCATTTGGCATGGAAGTCAACCTTCGGG 29090

QY 601 AACATGGCTGACTTATCATGGAGCCATTAATTTGGATGACAAAGATCCCAATTTCAAAGA 660
DB 29091 AACATGGCTGACTTATCATGGAGCCATTAATTTGGATGACAAAGATCCCAATTTCAAAGA 29150

QY 661 CAACTGCTACTCTGCAAGCAAGCAGTATGACGATCAAAAACATTTCCACCAACAGAGCC 720
DB 29151 CAACTGCTACTCTGCAAGCAAGCAGTATGACGATCAAAAACATTTCCACCAACAGAGCC 29210

QY 721 TAAAAAGGCAAAAAGAAAAGACTGATGAAGCTCAGCCCTTTGGCCGAGAGACAAAGAA 780
DB 29211 TAAAAAGGCAAAAAGAAAAGACTGATGAAGCTCAGCCCTTTGGCCGAGAGACAAAGAA 29270

QY 781 GCAGCCCACTGTGACTTCTTCTCTCGGCTGACATGGATGATTTCTCCAGACAACTTCA 840
DB 29271 GCAGCCCACTGTGACTTCTTCTCTCGGCTGACATGGATGATTTCTCCAGACAACTTCA 29330

QY 841 AAATTCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATGACCA 900
DB 29331 AAATTCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATGACCA 29390

QY 901 ACAAGCAGATGGGCTATGTAAACGTTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 960

Db 28911 CAACGTCACCTCAAGCAATTTGGGAGACGTGGTCCAGAAACAAACCCAAAGGAAATTTTCGGGGA 28970
QY 481 CCAAGACCTAATCAGACAAGGAACATGATTAACAAACATTTGGCGCGGCAAAATTTGCAAAATTTGC 540
Db 28971 CCAAGACCTAATCAGACAAGGAACATGATTAACAAACATTTGGCGCGGCAAAATTTGCAAAATTTGC 29030
QY 541 TCCAAGTGCCTCTGCATTTCTTTGGAAATGTCACGCAATTTGGCATGGAAGTCAACACCTTTCCGG 600
Db 29031 TCCAAGTGCCTCTGCATTTCTTTGGAAATGTCACGCAATTTGGCATGGAAGTCAACACCTTTCCGG 29090
QY 601 AACATGGCTGACTTATCATGAGCCCAATTAATTTGGATGACAAAGATCCACAAATTTCAAAGA 660
Db 29091 AACATGGCTGACTTATCATGAGCCCAATTAATTTGGATGACAAAGATCCACAAATTTCAAAGA 29150
QY 661 CAACTGCATCTGCTGAAACAGCACAATGACGCATACAAAACATTTCCCAACCAAGAGCC 720
Db 29151 CAACTGCATCTGCTGAAACAGCACAATGACGCATACAAAACATTTCCCAACCAAGAGCC 29210
QY 721 TAAAAAGGACAAAAAAGAAAGACATGATGAAGCTCAGGCTTTTGGCGCAGAGACAAAAAGAA 780
Db 29211 TAAAAAGGACAAAAAAGAAAGACATGATGAAGCTCAGGCTTTTGGCGCAGAGACAAAAAGAA 29270
QY 781 GCAGCCCACTGTGACTCTTTCTCTCGGCTGACATGGATGATTTCTCCAGACAACTTCA 840
Db 29271 GCAGCCCACTGTGACTCTTTCTCTCGGCTGACATGGATGATTTCTCCAGACAACTTCA 29330
QY 841 AAATTCATGATGAGCTTCTGCTGATTAACACTCAGGCATTAACACTCATGATGACCCAC 900
Db 29331 AAATTCATGATGAGCTTCTGCTGATTAACACTCAGGCATTAACACTCATGATGACCCAC 29390
QY 901 ACAAGGCAGATGGCTATGTAACGTTTTTCGCAATTTCCGTTTACGATACATGCTACTC 960
Db 29391 ACAAGGCAGATGGCTATGTAACGTTTTTCGCAATTTCCGTTTACGATACATGCTACTC 29450
QY 961 TTGTGCAGAAATGAAATTTCTGTAACATAACAGCACAAAGTAGTGTAACTTTAACTTAACTC 1020
Db 29451 TTGTGCAGAAATGAAATTTCTGTAACATAACAGCACAAAGTAGTGTAACTTTAACTTAACTC 29510
QY 1021 ACATAGCAATCTTTAATCAATGTGTAACATTTAGGAGGACCTTGAAGAGCCACCACTTT 1080
Db 29511 ACATAGCAATCTTTAATCAATGTGTAACATTTAGGAGGACCTTGAAGAGCCACCACTTT 29570
QY 1081 TCATCAGGCCACCGGAGTACGATCGAGGGTACAGTGAATTAATGCTAGGGAGAGC 1136
Db 29571 TCATCAGGCCACCGGAGTACGATCGAGGGTACAGTGAATTAATGCTAGGGAGAGC 29626

RESULT 13

US-10-839-729-16
; Sequence 16, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; PRIOR FILING DATE: 2004-05-04
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 29742
; TYPE: DNA
; ORGANISM: SARS Coronavirus
US-10-839-729-16

Query Match 100.0%; Score 1136; DB 18; Length 29742;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGCATCGTATGGTTGCAACTGAGGAGCCTTGAATACACCCAAAGACCAATTTGGCAGC 60

Db 28506 AGGCATCGTATGGTTGCAACTGAGGAGCCTTGAATACACCCAAAGACCAATTTGGCAGC 28565
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Db 28566 CCGCAATCTTAATAACAATGCTGCCACCGTGTACAACTTCTCTAGAGAAACAATTTGCC 28625
QY 121 AAAAGGCTTCTACGACAGAGGAAGCAGAGGGCGGAGTCAAGCCTTCTCGTCTCTCATC 180
Db 28626 AAAAGGCTTCTACGACAGAGGAAGCAGAGGGCGGAGTCAAGCCTTCTCGTCTCTCATC 28685
QY 181 ACGTAGTCCGCGTAATTTCAAGAAATTTCAACTCTCTGGCAGCAGTAGGGGAAATTTCTCTGC 240
Db 28686 ACGTAGTCCGCGTAATTTCAAGAAATTTCAACTCTCTGGCAGCAGTAGGGGAAATTTCTCTGC 28745
QY 241 TCGAATGCTAGCGGAGTGTGAAACTGCGCTCTCGCGTATTTGCTGTAGACAGATTTGAA 300
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Db 28806 CCAGCTTCAGAGCAAAAGTTTCTGGTAAAGGCCAACAAACAAAGGCCAAACTGTCACTAA 28865
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Db 28866 GAAATCTCTGCTGAGGCACTCTAAAAAGCCTCGCCAAAAACGTACTGCCACAAAAACAGTA 28925
QY 421 CAACTGCTCAAGCATTTGGGAGACGTGGTCCAGAACAAAAACCCAAAGGAAATTTTCGGGA 480
Db 28926 CAACTGCTCAAGCATTTGGGAGACGTGGTCCAGAACAAAAACCCAAAGGAAATTTTCGGGA 28985
QY 481 CCAGACCTAATCAGACAAGCACTGATTACAAACATTTGGCGGCAAAATTTGCACAAATTTGC 540
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QY 541 TCCAAGTGCCTCTGCAATTTTGGAAATGTCACGCAATTTGGCATGGAAGTCAACCTTCGGG 600
Db 29046 TCCAAGTGCCTCTGCAATTTTGGAAATGTCACGCAATTTGGCATGGAAGTCAACCTTCGGG 29105
QY 601 AACATGGCTGACTTATCATGAGGCCATTTAAATTTGGATGACAAAGATCCACAAATTTCAAAGA 660
Db 29106 AACATGGCTGACTTATCATGAGGCCATTTAAATTTGGATGACAAAGATCCACAAATTTCAAAGA 29165
QY 661 CAACTGCATCTGCTGAAACAAGCACAATTTGACGATACAAAAACATTTCCCAACCAAGAGCC 720
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QY 721 TAAAAAGGACAAAAAAGAAAGACCTGATGAAGCTCAGCCTTTTGGCGCAGAGACAAAAAGAA 780
Db 29226 TAAAAAGGACAAAAAAGAAAGACCTGATGAAGCTCAGCCTTTTGGCGCAGAGACAAAAAGAA 29285
QY 781 GCAGCCCACTGTGACTCTTTCTCTCGGCTGACATGGATGATTTCTCCAGACAACTTCA 840
Db 29286 GCAGCCCACTGTGACTCTTTCTCTCGGCTGACATGGATGATTTCTCCAGACAACTTCA 29345
QY 841 AAATTCATGATGAGGCTTCTGCTGATTTCAACTCAGCATAAAACACTCATCATGACCAAC 900
Db 29346 AAATTCATGATGAGGCTTCTGCTGATTTCAACTCAGCATAAAACACTCATCATGACCAAC 29405
QY 901 ACAAGGCAGATGGGCTATGTAACGTTTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 960
Db 29406 ACAAGGCAGATGGGCTATGTAACGTTTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 29465
QY 961 TTGTGCAGAAATGAAATTTCTCGTAACATAACAGCAGCAAGTAGTTTAACTTTAACTTCTC 1020
Db 29466 TTGTGCAGAAATGAAATTTCTCGTAACATAACAGCAGCAAGTAGTTTAACTTTAACTTCTC 29525
QY 1021 ACATAGCAATCTTTAATCAATGTGTAACATTTAGGAGGACCTTGAAGAGCCACCACTTT 1080
Db 29526 ACATAGCAATCTTTAATCAATGTGTAACATTTAGGAGGACCTTGAAGAGCCACCACTTT 29585
QY 1081 TCATCAGGCCACCGGAGTACGATCGAGGGTACAGTGAATTAATGCTAGGGAGAGC 1136

Db 29586 TCATCGAGGCCACGGGAGTACGATCGAGGTACAGTGAATAATGCTAGGGAGAGC 29641

RESULT 14

US-10-808-187-15

; Sequence 15, Application US/10808187

; Publication No. US2005000909A1

; GENERAL INFORMATION:

; APPLICANT: PEIRIS, JOSEPH S. M.

; APPLICANT: YUEN, KWOK YUNG

; APPLICANT: POON, LIT MAN

; APPLICANT: GUAN, YI

; APPLICANT: CHAN, KWOK HUNG

; APPLICANT: NICHOLLS, JOHN

; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE

; TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)

; FILE REFERENCE: V9661.0078

; CURRENT APPLICATION NUMBER: US/10/808,187

; PRIOR FILING DATE: 2004-03-24

; PRIOR APPLICATION NUMBER: 60/457,031

; PRIOR FILING DATE: 2003-03-24

; PRIOR APPLICATION NUMBER: 60/457,730

; PRIOR FILING DATE: 2003-03-26

; PRIOR APPLICATION NUMBER: 60/459,931

; PRIOR FILING DATE: 2003-04-02

; PRIOR APPLICATION NUMBER: 60/460,357

; PRIOR FILING DATE: 2003-04-03

; PRIOR APPLICATION NUMBER: 60/461,265

; PRIOR FILING DATE: 2003-04-08

; PRIOR APPLICATION NUMBER: 60/462,805

; PRIOR FILING DATE: 2003-04-14

; PRIOR APPLICATION NUMBER: 60/468,139

; PRIOR FILING DATE: 2003-05-05

; PRIOR APPLICATION NUMBER: 60/464,886

; PRIOR FILING DATE: 2003-04-23

; PRIOR APPLICATION NUMBER: 60/471,200

; PRIOR FILING DATE: 2003-05-16

; NUMBER OF SEQ IDS: 2476

; SOFTWARE: PatentIn ver. 3.2

; SEQ ID NO 15

; LENGTH: 29742

; TYPE: DNA

; ORGANISM: Human severe acute respiratory system virus

US-10-808-187-15

Query Match 100.0%; Score 1136; DB 19; Length 29742;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCATCGTATGGTTGCAACTGAGGGAGCCTTTGAATACACCCAAAGACCAATTTGGCAC 60

Db 28506 AGGCATCGTATGGTTGCAACTGAGGGAGCCTTTGAATACACCCAAAGACCAATTTGGCAC 28565

QY 61 CGCAATCTCTAATAACATGCTGCCACCGTGTACAACTTCTCAAGGAACAACATTTGCC 120

Db 28566 CGCAATCTCTAATAACATGCTGCCACCGTGTGTACAACTTCTCAAGGAACAACATTTGCC 28625

QY 121 AAAAGCTTCTACGACAGGGAGGAGGAGCGGAGCTCAAGCCTTTCTCGCTCTCTCATC 180

Db 28626 AAAAGCTTCTACGACAGGGAGGAGGAGCGGAGCTCAAGCCTTTCTCGCTCTCTCATC 28685

QY 181 AGCTAGTCGGGTAAATTCAAGAAATTTCAACTCTCGCAGCAGTAGGGGAAATTTCTCTGC 240

Db 28686 AGCTAGTCGGGTAAATTCAAGAAATTTCAACTCTCGCAGCAGTAGGGGAAATTTCTCTGC 28745

QY 241 TCGAATGGCTAGCGGAGGTGGTGAATCTGCCCTCGCGCTATTGCTGCTAGACAGATTGAA 300

Db 28746 TCGAATGGCTAGCGGAGGTGGTGAATCTGCCCTCGCGCTATTGCTGCTAGACAGATTGAA 28805

QY 301 CCAGCTTTAGACCAAGTTTCTGGTAAAGCCCAACCAACAGGCGCAACTGTCACTAA 360

Db 28806 CCAGCTTTAGACCAAGTTTCTGGTAAAGCCCAACCAACAGGCGCAACTGTCACTAA 28865

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Db 28866 GAAATCTGCTGTAGGCAATCTAAAAAGCCTCGCCAAAAACGTAACGTAACGTAACGTA 28925

QY 421 CAACGTCACCTCAAGCAATTTGGGAGAGCGTGTCCAGACAAACCCCAAGGAAATTTCCGGGA 480

Db 28926 CAACGTCACCTCAAGCAATTTGGGAGAGCGTGTCCAGACAAACCCCAAGGAAATTTCCGGGA 28985

QY 481 CCAAGACCTTAATCAGACAAAGGAACCTGATTAACAACATTTGGCCCGCAATTTGCACAAATTTGC 540

Db 28986 CCAAGACCTTAATCAGACAAAGGAACCTGATTAACAACATTTGGCCCGCAATTTGCACAAATTTGC 29045

QY 541 TCCAAGTGCCTCTGCATTTCTTTGGAATGTACGCAATTTGGCAATTTGGCAATTTGGCAATTTGGC 600

Db 29046 TCCAAGTGCCTCTGCATTTCTTTGGAATGTACGCAATTTGGCAATTTGGCAATTTGGCAATTTGGC 29105

QY 601 AACATGGCTGACTTATCATGGAGCCATTAAATTTGGATGACAAAGATCCCAATTTCAAAGA 660

Db 29106 AACATGGCTGACTTATCATGGAGCCATTAAATTTGGATGACAAAGATCCCAATTTCAAAGA 29165

QY 661 CAACGTCATCTGCTGGAACAAGCACAATTGACGCATACAAAAACATTTCCCAACCAAGAGCC 720

Db 29166 CAACGTCATCTGCTGGAACAAGCACAATTGACGCATACAAAAACATTTCCCAACCAAGAGCC 29225

QY 721 TAAAAAGGACAAAAAGAAAAAGAGCTGATGAAGCTCAGCCCTTTGCGCGCAGAGACAAAGAA 780

Db 29226 TAAAAAGGACAAAAAGAAAAAGAGCTGATGAAGCTCAGCCCTTTGCGCGCAGAGACAAAGAA 29285

QY 781 GCAGCCCACTGTGACTCTTTCTTCCGCGCTGACATGGATGATTTCTCCAGACCACTTCA 840

Db 29286 GCAGCCCACTGTGACTCTTTCTTCCGCGCTGACATGGATGATTTCTCCAGACCACTTCA 29345

QY 841 AAATTCATGAGTGGAGCTTCTGCTGATTAACACTCAGGCATAAACACTCATGATGACCAC 900

Db 29346 AAATTCATGAGTGGAGCTTCTGCTGATTAACACTCAGGCATAAACACTCATGATGACCAC 29405

QY 901 ACAAGCAGATGGCTATGTAACCGTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 960

Db 29406 ACAAGCAGATGGCTATGTAACCGTTTTCGCAATTTCCGTTTACGATACATAGTCTACTC 29465

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Db 29526 ACATAGCAATCTTTAATCAATGTGTAACTTAAAGGAGGAGCTTGAAGAGCCACCACTTT 29585

QY 1081 TCATCGAGGCCACGGGAGTACGATCGAGGGTACAGTGAATTAATGCTAGGGAGAGC 1136

Db 29586 TCATCGAGGCCACGGGAGTACGATCGAGGGTACAGTGAATTAATGCTAGGGAGAGC 29641

RESULT 15

US-10-808-187-16

; Sequence 16, Application US/10808187

; Publication No. US2005000909A1

; GENERAL INFORMATION:

; APPLICANT: PEIRIS, JOSEPH S. M.

; APPLICANT: YUEN, KWOK YUNG

; APPLICANT: POON, LIT MAN

; APPLICANT: GUAN, YI

; APPLICANT: CHAN, KWOK HUNG

; APPLICANT: NICHOLLS, JOHN

; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE

; TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)

; FILE REFERENCE: V9661.0078

; CURRENT APPLICATION NUMBER: US/10/808,187

; CURRENT FILING DATE: 2004-03-24

; PRIOR APPLICATION NUMBER: 60/457,031

; PRIOR FILING DATE: 2003-03-24

; PRIOR APPLICATION NUMBER: 60/457,730

; PRIOR FILING DATE: 2003-03-26

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; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 16
; LENGTH: 29742
; TYPE: DNA
; ORGANISM: Human severe acute respiratory system virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(29742)
US-10-808-187-16

Query Match      100.0%; Score 1136; DB 19; Length 29742;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGGCATCGTATGGGTGCAACTGAGGAGCCTTGAATACACCAAGACCAACATTGGCAC 60
DB      28506 AGGCATCGTATGGGTGCAACTGAGGAGCCTTGAATACACCAAGACCAACATTGGCAC 28505

QY      61 CCGCAATCCTAATAAACAATGTCGCCACCGTGTCTACAACTTCTCAAGGAACAACATTGCC 120
DB      28566 CCGCAATCCTAATAAACAATGTCGCCACCGTGTCTACAACTTCTCAAGGAACAACATTGCC 28525

QY      121 AAAAGGCTTACGACAGAGGAGGAGGAGGCGGAGTCAAGCCTCTTCTCGCTCTCATC 180
DB      28626 AAAAGGCTTCTACGACAGAGGAGGAGGCGGAGTCAAGCCTCTTCTCGCTCTCATC 28685

QY      181 ACCTAGTCGCGGTAATTCAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCCTCTGC 240
DB      28686 ACCTAGTCGCGGTAATTCAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCCTCTGC 28745

QY      241 TCGAATGGCTACGCGAGGTGGTGAAACTGCCCTTCGCGCTATTGCTGTAGACAGATTGAA 300
DB      28746 TCGAATGGCTACGCGAGGTGGTGAAACTGCCCTTCGCGCTATTGCTGTAGACAGATTGAA 28805

QY      301 CCAGCTTGAGAGCAAGTTTCTGTTAAGGCCAACAACAAGGCCCAAACTGTCACTAA 360
DB      28806 CCAGCTTGAGAGCAAGTTTCTGTTAAGGCCAACAACAAGGCCCAAACTGTCACTAA 28865

QY      361 GAAATCTGCTGTAGGCAATCTAAAAGCCTGCCAAAACCGTACTGCCACAAAACAGTA 420
DB      28866 GAAATCTGCTGTAGGCAATCTAAAAGCCTGCCAAAACCGTACTGCCACAAAACAGTA 28925

QY      421 CAACGTCACCTCAAGCATTTGGGAGACGTGGTCCAGAACAAACCCAAAGGAAATTCGGGA 480
DB      28926 CAACGTCACCTCAAGCATTTGGGAGACGTGGTCCAGAACAAACCCAAAGGAAATTCGGGA 28985

QY      481 CCAAGACCTAATCAGACAGGAACTGATTACAAACNTTGGCGCCAAATTGCACAATTTGC 540
DB      28986 CCAAGACCTAATCAGACAGGAACTGATTACAAACNTTGGCGCCAAATTTGC 29045

QY      541 TCCAAGTGCCTCTGCAATCTTTGGAATGTCAAGCATGGCAGTCAACACCTTCGGG 600
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QY      601 AACATGGCTGACTTATCATGGAGCCCAATTAATTTGGATGACAAAGATCCAATTTCAAGA 660
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QY      661 CAAGCTCATACTGCTGAACAAGACACATTTGACGCATACAAAAACATTTCCACCACACAGAGCC 720
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QY      721 TAAAAAGGACAAAAAGAAAAAGACTGTATGAAGCTCAGCCTTTGCCGACAGACAAAAGAA 780
DB      29226 TAAAAAGGACAAAAAGAAAAAGACTGTATGAAGCTCAGCCTTTGCCGACAGACAAAAGAA 29285

QY      781 GCAGCCCACTGTGACTCTTCTCTCGGCTGACATGGATGATTTCTCCAGACAACTTCA 840
DB      29286 GCAGCCCACTGTGACTCTTCTCTCGGCTGACATGGATGATTTCTCCAGACAACTTCA 29345

QY      841 AAATTCCATGATGGAGCTTCTGTGATTCAACTCAGGCATAAAACACTCATGATGACCCAC 900
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QY      901 ACAAGGCAGATGGGCTATGTAAACGTTTTTCGCAATTCGGTTTACGATACATAGTCTACTC 960
DB      29406 ACAAGGCAGATGGGCTATGTAAACGTTTTTCGCAATTCGGTTTACGATACATAGTCTACTC 29465

QY      961 TTGTGCAGAAATGAATTTCTCGTAACTTAACAGCACAAGTAGGTTAGTTAACTTTAATCTC 1020
DB      29466 TTGTGCAGAAATGAATTTCTCGTAACTTAACAGCACAAGTAGGTTAGTTAACTTTAATCTC 29525

QY      1021 ACATAGCAATCTTTAATCAATGTGTAACTTAGGGAGGACTTTGAAAGAGCCACCACTTT 1080
DB      29526 ACATAGCAATCTTTAATCAATGTGTAACTTAGGGAGGACTTTGAAAGAGCCACCACTTT 29585

QY      1081 TCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGTGAATAATGCTTAGGGAGAGC 1136
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Job time : 843.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2005, 11:03:36 ; Search time 5001.54 Seconds
(without alignments)
8645.536 Million cell updates/sec

Title: US-10-764-075-1
Perfect score: 1136
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	43.2	3.8	769	6 CB669132	CB669132 OSJNE01G
C 2	43	3.8	323	7 H55033	H55033 HHU58b Soxg
C 3	42.8	3.8	640	4 BJ328127	BJ328127 BJ328127
C 4	42.4	3.7	1101	9 CNS00L00	AL088607 Drosophil
C 5	42.2	3.7	434	4 BJ358542	BJ358542 BJ358542
C 6	42.2	3.7	518	2 BF598760	BF598760 sv21d10.y
C 7	42.2	3.7	540	4 BJ362480	BJ362480 BJ362480
C 8	42.2	3.7	556	4 BJ366773	BJ366773 BJ366773
C 9	42.2	3.7	593	4 BJ328471	BJ328471 BJ328471
C 10	42.2	3.7	601	4 BJ339144	BJ339144 BJ339144
C 11	42.2	3.7	605	4 BJ365525	BJ365525 BJ365525
C 12	42.2	3.7	606	4 BJ339537	BJ339537 BJ339537
C 13	42.2	3.7	616	4 BJ387757	BJ387757 BJ387757
C 14	42.2	3.7	617	4 BJ366277	BJ366277 BJ366277
C 15	42.2	3.7	629	4 BJ370135	BJ370135 BJ370135
C 16	42.2	3.7	656	4 BJ361324	BJ361324 BJ361324
C 17	42	3.7	532	5 BX512459	BX512459 BX512459
C 18	42	3.7	583	4 BJ333936	BJ333936 BJ333936
C 19	42	3.7	632	2 BB623030	BB623030 BB623030
C 20	42	3.7	772	5 BU558830	BU558830 AGENCOURT
C 21	42	3.7	780	9 AY400589	AY400589 Mus muscu
C 22	42	3.7	1002	6 BY708644	BY708644 BY708644
C 23	42	3.7	1411	3 AK008741	AK008741 Mus muscu
C 24	42	3.7	1532	3 AK017592	AK017592 Mus muscu

25	42	3.7	2310	3 AK032624	AK032624 Mus muscu
26	42	3.7	2718	3 AK032314	AK032314 Mus muscu
C 27	42	3.7	3658	3 AK083404	AK083404 Mus muscu
C 28	41.6	3.7	536	4 BJ387830	BJ387830 BJ387830
C 29	41.4	3.6	300	8 AZ254800	AZ254800 p050.K19L
C 30	41.4	3.6	777	9 AG477863	AG477863 Mus muscu
31	41.4	3.6	834	9 CNS0112M	AL099736 Drosophil
32	41.4	3.6	1049	9 CNS001W5	AL075516 Drosophil
C 33	41.4	3.6	1101	9 CNS00L72	AL078714 Drosophil
C 34	40.8	3.6	922	9 CNS0073W	AL066784 Drosophil
35	40.6	3.6	467	2 BF286190	BF286190 EST450781
36	40.6	3.6	517	2 BF566518	BF566518 UI-R-800-
37	40.6	3.6	558	2 AW919227	AW919227 EST350531
C 38	40.6	3.6	723	8 BH961520	BH961520 Ood50g10.
C 39	40.6	3.6	1117	8 CC227680	CC227680 CH261-44M
40	40.4	3.6	463	1 AI060840	AI060840 ub44e06.r
C 41	40.2	3.5	294	2 BB125565	BB125565 BB125565
42	39.8	3.5	353	6 CA780863	CA780863 MFLJ3847
43	39.8	3.5	693	4 BG644557	BG644557 EST506176
C 44	39.8	3.5	747	9 AG375742	AG375742 Mus muscu
45	39.8	3.5	779	9 CNS04A9H	AL281582 Tetraodon

ALIGNMENTS

RESULT 1 CB669132/c
LOCUS CB669132 769 bp mRNA linear EST 09-APR-2003
DEFINITION OSJNE01G10.f OSJNEE Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEE01G10 5', mRNA sequence.

ACCESSION CB669132
VERSION CB669132.1 GI:29672857
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE 1 (bases 1 to 769)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

TITLE Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 01 row: G column: 10
Seq primer: gta aaa cga cgg cca gtc.

FEATURES
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XhoI; 24 hrs after inoculation with Rice Blast (70-15)"

ORIGIN

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Best Local Similarity 48.8%; Pred. No. 0.55;
Matches 117; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 524 CAAATTGGACAAATTTGCTCCAGTCCCTCTGCAATCTTTTGGAAATGTCACGCATTTGGCATG 583
DB 444 CGACGTGCTAATCTTTGAGCAATTTTATGTTTTCCTTTGGTTGATCCCATCTCGTTT 385

QY 584 GAAGTCACACCTTCGGGAACATGCTGACTATATCATGGAGCATTAATAATTGGATGACAAA 643
DB 384 GGAATTACGCCATCAGCAAGAGCTACAAACAATCAATGTTAGATAAGCTATGATCAATGAT 325

QY 644 GATCCACAATTCAAAGACAACGTCATCTGCTGAACAGCATTGAGCGCATACAAACA 703
DB 324 ATTAAAAACGTCAAAGAGAACTAATCTACACAATAAATACTACAAAAAATCCAAAAT 265

QY 704 TCCCAACACAGAGCCCTAAAAGAGCAAAAAGAAAGAGACTGATGAAGCTCAGCCTTTG 763
DB 264 ATAAATCATATATGCTGCTTAATAGATAAAGCTATATTTTTCAGAGGTCAAACTTTG 205

RESULT 2
H55033/c
LOCUS H55033 323 bp mRNA linear EST 27-SEP-1999
DEFINITION HHU58b Sorghum bicolor cv. TX430 Sorghum bicolor cDNA clone HHU58
3' similar to transketolase, chloroplast (TKLC1), mRNA sequence.
ACCESSION H55033
VERSION H55033.1 GI:2674237
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 323)
AUTHORS Wyrich,R., Dressen,U., Brockmann,S., Streubel,M., Chang,C.,
Qiang,D., Paterson,A.H. and Westhoff,P.
TITLE The molecular basis of C4 photosynthesis in sorghum: isolation,
characterization and RFLP mapping of mesophyll- and
bundle-sheath-specific cDNAs obtained by differential screening
JOURNAL Plant Mol. Biol. 37 (2), 319-335 (1998)
MEDLINE 98278366
PUBMED 9617804
COMMENT On Dec 10, 1997 this sequence version replaced gi:1000813.
Contact: Westhoff P
Plant Molecular Biology
Heinrich-Heine-University
Universitaetsstrasse 1, D-40225 Duesseldorf, Germany
Tel: (49)-211-311-2338
Fax: (49)-211-311-4871
Email: west@uni-duesseldorf.de
Homology: sp/p22976, Blastx-Score: 176, pval: 2.1e-29
Seq primer: M13 (-20).
FEATURES
Location/Qualifiers
source 1..323
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Best Local Similarity 52.6%; Pred. No. 0.48;
Matches 91; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 627 TTAAATTTGGATGACAAAGATCCAAATTCAAAGACAACCTCATCTGCTGTAACAAGCACA 686
DB 313 TTTTTCGAAGAAATAATACATCATCATTTATGAGCTCAATATATATAATGTTATGTACCAT 254

Query Match          3.8%; Score 42.8; DB 4; Length 640;
Best Local Similarity 48.2%; Pred. No. 0.68;
Matches 119; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 412 AAAACAGTACAACAGTCCTCAAGCATTTGGGAGAGCTGGTCAGAAACAAACCCAAAGGAAA 471
DB 275 AACAAAACAGGTGGTTAAACAATGATTTTGGATTACTTGGACCTGCAATTACACCACTTAA 216

QY 472 TTTCGGGACCAAGACCTTAATCAGACAAGGAACCTGATTACAAACATTGGCCGCAAAATGCG 531
DB 215 AGATTTTGGAAATCAAAACCAATGCTTAAGTCAATAGATTGACCACTGTTTACGAAATTTAC 156

QY 532 ACAATTTGCTCCAAGTGCCTGCAATCTTTGGATGTGTCACCATTTGGCATGGAAGTCAC 591
DB 155 CAAATTTGCACCAAGTTGAAGTGAATCATTTTGGAAATTAACAATCAATTTCTAACTGGGAA 96

QY 592 ACCTTCGGGAACATGGCTGACTTATCATGGAGCCATTAATTTGGATGACAAAGATCCACA 651
DB 95 ACCTGGTTGTAACCACTGAATGACCATCTACCATTTTAATCGGTTGTAACGGTTTCCAAA 36

QY 652 ATTCAAA 658
DB 35 GAGGAAA 29

RESULT 4
CNS00LOO
LOCUS CNS00LOO 1101 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:

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RESULT 5
BJ358542/c
LOCUS
DEFINITION BJ358542 Dictyostelium discoideum cDNA library, CF Dictyostelium
 discoideum cDNA clone ddc10f01 5', mRNA sequence.
ACCESSION BJ358542
KEYWORDS BJ358542.1 GI:19258137
SOURCE Est.
ORGANISM Dictyostelium discoideum
REFERENCE Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
AUTHORS 1 (bases 1 to 434)
 Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the culmination
 stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
FEATURES Location/Qualifiers
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 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 389 AACAAAACAGGTGTTACAAATGATTTTGGATTACTTGGACCTGCATTTACACCAGTTAA 330
 Qy 472 TTTCCGGGGACCAAGACCTATACAGAACGATGATTACAAACATGGCGCGCAATTGC 531
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 329 AGATTTTGGAAATCAAAACCAATGCTTAAGTCAATAGATTGACCACTGTTACGAAATTTAC 270
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 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 269 CAAATTTGCACCAAGTTGAAGTGAATCATTTGGANTTACAACTCAATTTCTAATCGGAA 210
 Qy 592 ACCTTCGGGAACATGGCTGCTATCATGAGGCATTTAAATTTGGATGACAAAGATCCACA 651
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 209 ACCTGGTTGTAAACCACTGAATGACCATTCACCATTTGAATCGTTGTAACGGTTCCAAA 150
 Qy 652 ATTCAA 658
 Db ||||
 149 GAGGAA 143
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LOCUS
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ACCESSION BF598760
KEYWORDS BF598760.1 GI:11691084
SOURCE Est.
ORGANISM Glycine soja
 Glycine soja
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 518)

Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterson,R. and Wilson,R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) High quality sequence stop: 421.

Location/Qualifiers

1. 518

/organism="Glycine soja"

/mol_type="mRNA"

/db_xref="taxon:3848"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl057-187"

/tissue_type="Degenerating cotyledons, 2 week old seedling"

/lab_host="DH10B"

/clone_lib="Gm-cl057"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 2 week old seedlings from PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 3.7%; Score 42.2; DB 2; Length 518;
Best Local Similarity 54.1%; Pred. No. 0.96;
Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 622 ACCGATTAAATGGATGACAAAGATCCCAATTCAAAGACACGTCATCTGCTGAACAA 681
Db |||||
332 AGCAAGCAATTAAGTGACACAAAGATACAGATAGTAAACTTACCATCTACTGCAAAACGA 273
QY 682 GCACATTGCGATACAAAGACATTCACCACACAGGCTTAAAGGACAAAAGAAA 741
Db |||||
272 GCCAATCTAGAAGCTCCCATCTCTTTTGAACAGGGATCCTTGACACGCAAAAGCGAAACA 213
QY 742 GACTGATGAAGCTCAGGCTTTTCCCGCAGACAGACAAAGAA 780
Db |||||
212 GACTGTTCATCAAAATCTCTCCCATATAGGAAGAAA 174

RESULT 7

BJ362480/c
LOCUS 540 bp mRNA linear EST 07-MAR-2002
DEFINITION Dictyostelium discoideum cDNA library, CP Dictyostelium
discoideum cDNA clone ddc22a02 5', mRNA sequence.
ACCESSION BJ362480
VERSION BJ362480.1 GI:19262075
KEYWORDS EST.
SOURCE Dictyostelium discoideum

ORGANISM

Dictyostelium discoideum

Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 540)

Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the culmination stage

JOURNAL

Unpublished (2002)

Contact: Tadao Shin-i

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Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

source

1. 540

/organism="Dictyostelium discoideum"

/mol_type="mRNA"

/strain="AX4"

/db_xref="taxon:44689"

/clone="ddc22a02"

/sex="mat A"

/dev_stage="Culmination stage"

/clone_lib="Dictyostelium discoideum cDNA library, CF"

ORIGIN

Query Match 3.7%; Score 42.2; DB 4; Length 540;
Best Local Similarity 48.2%; Pred. No. 0.97;
Matches 119; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 412 AAAACAGTACAACTCACTCAAGCATTTGGGAGACGTTGGTCCAGAACAAACCCAGGAAA 471
Db |||||
527 AACAAACAGGTGTACAAATGATTTGGATTACTTGGACCTGCATTTACACCACTTAA 468
QY 472 TTTCGGGACCAAGACCTTAATCAGACAAAGAACTGATTAACAAACATTCGCGCAAAATTCG 531
Db |||||
467 AGATTTTGGAAATCAACCAATGCTTAAGTCAATAGATTGACCACTGTTACGAAATTTAC 408
QY 532 ACAATTTGCTCAAGTGCCTCTGCATCTTTGGATGTGCACGATTCGATGGAGATCAC 591
Db |||||
407 CAATTTGTCACCACTGTTGAAGTGAATCATTTGGAAATTAACAACTCAATTCCTAATCTGGGAA 348
QY 592 ACCTTCGGGAACATGGCTGACTTATCATGAGAGCCATTAATTTGGATGACAAAGATCCACA 651
Db |||||
347 ACCTGTTGTTAAACCACTGAATGACCATCTATCATTCGTTGTAACGGTTCCAAA 288
QY 652 ATTCAAA 658
Db |||||
287 GAGGAAA 281

RESULT 8

BJ366773/c

LOCUS

DEFINITION BJ366773 Dictyostelium discoideum cDNA library, linear EST 08-MAR-2002
discoideum cDNA clone ddc40a04 5', mRNA sequence.

ACCESSION BJ366773

VERSION BJ366773.1 GI:19276075

KEYWORDS EST.

SOURCE

Dictyostelium discoideum

Dictyostelium discoideum

Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 556)

Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.

Full length cDNA of Dictyostelium discoideum at the culmination stage

Unpublished (2002)

Contact: Tadao Shin-i

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FEATURES
source
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .556

/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddc4004"
/sex="mat A"
/dev_stage="Culmination stage"
/clone_lib="Dictyostelium discoideum cDNA library, CF"

ORIGIN

Query Match 3.7%; Score 42.2; DB 4; Length 556;
Best Local Similarity 48.2%; Pred. No. 0.98;
Matches 119; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 412 AAAACAGTACACGTCACCTCAAGCACTTTGGAGACGCTGGTCCAGAACCAACCCAGGAAA 471

DB 457 AACAAAACAGGTGGTAACAAATGATTTGGATTACTTTGGACCTGCAATTTACACCAAGTTAA 398

QY 472 TTTCCGGGACCAAGACCTTAATCAGACAAGGAAGTGAATACAAACATTTGGCCGCAAAATTGC 531

DB 397 AGATTTTGGAAATCAACCAATGCTTAAGTCAATAGATTGACCACTGTTACGAAATTTAC 338

QY 532 ACAATTTGCTCCAAAGTGCCTCTGCATTTCTTTGGAATGTCAAGCATTTGGCATGGAAAGTCAC 591

DB 337 CAAATTTGCACCAAGTTGAAGTGAATCAATTTGGAATTAACAACTCAATTTCACTGCGAA 278

QY 592 ACCTTCGGGAACATGCTGACCTATCATGAGGACCTTAATTTGGATGACAAAGATCCACA 551

DB 277 ACCTGGTTGTAACCACTGAATGACCATCTACCAATTTGAATCGGTTGTAACGGTTCCAAA 218

QY 652 ATTCAAA 658

DB 217 GAGGAAA 211

RESULT 9

BJ328471/c
LOCUS
DEFINITION
Accession
Version
Keywords
Source
Organism
Reference
Authors
Title
Journal
Comment

BJ328471 593 bp mRNA linear EST 05-MAR-2002
Dictyostelium discoideum cDNA library, AF Dictyostelium
discoideum cDNA clone dda28e11 5', mRNA sequence.

Accession
Version
Keywords
Source
Organism

BJ328471.1 .GI:19158601
Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

Reference
Authors
Title
Journal
Comment

1 (bases 1 to 593)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
stage

Unpublished (2002)
Contact: Tadasu Shin-i
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Location/Qualifiers
1. .593

FEATURES

source

/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="dda28e11"
/sex="mat A"
/dev_stage="Aggregation stage"
/clone_lib="Dictyostelium discoideum cDNA library, AF"

ORIGIN

Query Match 3.7%; Score 42.2; DB 4; Length 593;
Best Local Similarity 48.2%; Pred. No. 1;
Matches 119; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 412 AAAACAGTACACGTCACCTCAAGCACTTTGGAGACGCTGGTCCAGAACCAACCCAGGAAA 471

DB 303 AACAAAACAGGTGGTAACAAATGATTTGGATTACTTTGGACCTGCAATTTACACCAAGTTAA 244

QY 472 TTTCCGGGACCAAGACCTTAATCAGACAAGGAAGTGAATACAAACATTTGGCCGCAAAATTGC 531

DB 243 AGATTTTGGAAATCAACCAATGCTTAAGTCAATAGATTGACCACTGTTACGAAATTTAC 184

QY 532 ACAATTTGCTCCAAAGTGCCTCTGCATTTCTTTGGAATGTCAAGCATTTGGCATGGAAAGTCAC 591

DB 183 CAAATTTGCACCAAGTTGAAGTGAATCAATTTGGAATTAACAACTCAATTTCACTGCGAA 124

QY 592 ACCTTCGGGAACATGCTGACCTATCATGAGGACCTTAATTTGGATGACAAAGATCCACA 651

DB 123 ACCTGGTTGTAACCACTGAATGACCATCTACCAATTTGAATCGGTTGTAACGGTTCCAAA 64

QY 652 ATTCAAA 658

DB 63 GAGGAAA 57

RESULT 10

BJ339144/c

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

BJ339144 601 bp mRNA linear EST 07-MAR-2002

Dictyostelium discoideum cDNA library, AF Dictyostelium

discoideum cDNA clone dda64f10 5', mRNA sequence.

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

BJ339144.1 .GI:19247506

Dictyostelium discoideum

Dictyostelium discoideum

Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostelium discoideum at the aggregation

stage

Unpublished (2002)

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Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .601

/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="dda64f10"
/sex="mat A"
/dev_stage="Aggregation stage"
/clone_lib="Dictyostelium discoideum cDNA library, AF"

Query Match 3.7%; Score 42.2; DB 4; Length 601;
Best Local Similarity 48.2%; Pred. No. 1;
Matches 119; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 412 AAAACAGTACACGTCACCTCAAGCACTTTGGAGACGCTGGTCCAGAACCAACCCAGGAAA 471

DB 582 AACAAAACAGGTGGTAACAAATGATTTGGATTACTTTGGACCTGCAATTTACACCAAGTTAA 523

QY 472 TTTCCGGGACCAAGACCTTAATCAGACAAGGAAGTGAATACAAACATTTGGCCGCAAAATTGC 531

DB 522 AGATTTTGGAAATCAACCAATGCTTAAGTCAATAGATTGACCACTGTTACGAAATTTAC 463

QY 532 ACAATTTGCTCCAAAGTGCCTCTGCATTTCTTTGGAATGTCAAGCATTTGGCATGGAAAGTCAC 591


```
JOURNAL
COMMENT
Unpublished (2002)
Contact: Tadasu Shin-i
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Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1. .616
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="dds4a23"
/sex="mat A"
/dev_stage="slug stage"
/clone_lib="Dictyostelium discoideum cDNA library, SF"

ORIGIN
Query Match 3.7%; Score 42.2; DB 4; Length 616;
Best Local Similarity 48.2%; Pred. No. 1;
Matches 119; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

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Db 518 AACAAAAACAGGTGGTAAACAAATGATTTTGGATTACTTGGACCTGCAATTTACACCAAGTTAA 459
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QY 472 TTTCGGGGACCAAGACCTAATCAGACAGAACTGATTACAAACATTTGGCGGCAAAATTGC 531
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Db 458 AGATTTTGGAAATCAAAACCAATGCTTAAGTCAATAGATTGACCACTGTTAGGAATTTAC 399
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QY 532 ACAATTTGCTCCAAAGTGCCTCTGCAATCTTTTGAATGTTCACGCAATTTGGCATGGAAGTCAC 591
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Db 398 CAAATTTGCAACAGTTGAAAGTGAATCAATTTTGAATTTACAAACTCAATTTCTAACTGGGAA 339
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QY 652 ATTCAAA 658
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Db 278 GAGGAAA 272
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RESULT 15
BJ370135/c
LOCUS
DEFINITION
BJ370135 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc53d06 5', mRNA sequence.
ACCESSION
BJ370135
VERSION
BJ370135.1 GI:19279518
KEYWORDS
EST.
SOURCE
Dictyostelium discoideum
ORGANISM
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
1 (bases 1 to 629)
AUTHORS
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE
Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL
Unpublished (2002)
COMMENT
Contact: Tadasu Shin-i
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National Institute of Genetics
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1. .629
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddc53d06"
/sex="mat A"
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/clone_lib="Dictyostelium discoideum cDNA library, CF"

ORIGIN
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Best Local Similarity 48.2%; Pred. No. 1;
Matches 119; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

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RESULT 14
BJ366277/c
LOCUS
DEFINITION
BJ366277 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc38112 5', mRNA sequence.
ACCESSION
BJ366277
VERSION
BJ366277.1 GI:19275579
KEYWORDS
EST.
SOURCE
Dictyostelium discoideum
ORGANISM
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
1 (bases 1 to 617)
AUTHORS
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE
Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL
Unpublished (2002)
COMMENT
Contact: Tadasu Shin-i
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National Institute of Genetics
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1. .617
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"

JOURNAL
COMMENT
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1. .616
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="dds4a23"
/sex="mat A"
/dev_stage="slug stage"
/clone_lib="Dictyostelium discoideum cDNA library, SF"

ORIGIN
Query Match 3.7%; Score 42.2; DB 4; Length 616;
Best Local Similarity 48.2%; Pred. No. 1;
Matches 119; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 412 AAAACAGTACAAGCTCACTCAAGCATTTGGGACAGCTGGTCCAGAACAAACCCAGGAAA 471
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 516 AACAAAAACAGGTGGTAAACAAATGATTTTGGATTACTTGGACCTGCAATTTACACCAAGTTAA 457
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QY 472 TTTCGGGGACCAAGACCTAATCAGACAGAACTGATTACAAACATTTGGCGGCAAAATTGC 531
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Db 456 AGATTTTGGAAATCAAAACCAATGCTTAAGTCAATAGATTGACCACTGTTACGGAATTTAC 397
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 532 ACAATTTGCTCCAAAGTGCCTCTGCAATCTTTTGAATGTTCACGCAATTTGGCATGGAAGTCAC 591
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Db 396 CAAATTTGCAACAGTTGAAAGTGAATCAATTTTGAATTTACAAACTCAATTTCTAACTGGGAA 337
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QY 592 ACCTTCGGGAACATGCTGACTTATCATGGAGCCATTAATTTGGATGACAAAGATCCACA 651
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Db 336 ACCTGGTTGTAACCACTGAATGACCATCTACCATTTGAATCGGTTGTAAACGGTTCCAAA 277
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QY 652 ATTCAAA 658
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Db 276 GAGGAAA 270
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Db 571 AACAAAAACAGGTGGTAACAGATGATTTTGGATTACTTTGGACCTGCATTTACACCAGTTAA 512
QY 472 TTTCGGGGACCAAGACCTTAATCAGACAAGGAACCTGATTACAAAACATTTGGCCGCAAAATTGC 531
Db 511 AGATTTTGGGAATCAAAACCAATGCTTAAGTCAATAGATTGACCAACTGTTACGAAAATTTAC 452
QY 532 ACAATTTGCTCCCAAGTGCCTCTGCAATCTTTGGAATGTCACGCATTTGGCATGGAAGTCAC 591
Db 451 CAAATTTGCACCAGTTGAAGTGAATCATTTGGAATTAACAACCTCAATTCCTAAGTGGAA 392
QY 592 ACCTTCGGGAACATGGCTGACTTATCATGGAGCCCATTAATAATTGGATGACAAAGATCCACA 651
Db 391 ACCTGGTTGTAAACCACTGAATGACCATCTACCATTTGAATCGGTTGTAAACGGTTCCAAA 332
QY 652 ATTCAAA 658
Db 331 GAGGAAA 325

Search completed: May 15, 2005, 14:18:37
Job time : 5008.54 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2005, 11:00:45 ; Search time 95.9067 Seconds
(without alignments)
10609.895 Million cell updates/sec

Title: US-10-764-075-2

Perfect score: 21
Sequence: 1 atgaccacacaaggcagatgg 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	1669	14	AY536760 SARS coro
2	21	100.0	1873	14	AY534761 SARS coro
3	21	100.0	1938	14	AY534762 SARS coro
4	21	100.0	2304	14	AY322205 SARS coro
5	21	100.0	2810	14	AY290752 SARS coro
6	21	100.0	8439	14	AY304489 SARS coro
7	21	100.0	8581	14	AY304487 SARS coro
8	21	100.0	11006	14	AY304491 SARS coro
9	21	100.0	11010	14	AY304493 SARS coro
10	21	100.0	11010	14	AY304494 SARS coro
11	21	100.0	13471	14	AY304490 SARS coro
12	21	100.0	13471	14	AY304492 SARS coro
13	21	100.0	29013	14	AY463060 SARS coro
14	21	100.0	29350	14	AY394999 SARS coro
15	21	100.0	29350	14	AY395000 SARS coro
16	21	100.0	29350	14	AY395001 SARS coro
17	21	100.0	29350	14	AY395002 SARS coro
18	21	100.0	29433	14	AY394977 SARS coro
19	21	100.0	29530	14	AY394985 SARS coro

20	21	100.0	29573	14	AY338174	SARS coro
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22	21	100.0	29573	14	AY348314	SARS coro
23	21	100.0	29577	14	AY559094	SARS coro
24	21	100.0	29592	14	AY463059	SARS coro
25	21	100.0	29620	14	AY395004	SARS coro
26	21	100.0	29640	14	AY394978	SARS coro
27	21	100.0	29645	14	AY394979	SARS coro
28	21	100.0	29646	14	AY394982	SARS coro
29	21	100.0	29647	14	AY395003	SARS coro
30	21	100.0	29661	14	AY559086	SARS coro
31	21	100.0	29665	14	AY394988	SARS coro
32	21	100.0	29670	14	AY559082	SARS coro
33	21	100.0	29683	14	AY394996	SARS coro
34	21	100.0	29683	14	AY394997	SARS coro
35	21	100.0	29699	14	AY394983	SARS coro
36	21	100.0	29705	14	AY283795	SARS coro
37	21	100.0	29705	14	AY394980	SARS coro
38	21	100.0	29706	14	AY283797	SARS coro
39	21	100.0	29709	14	AY394987	SARS coro
40	21	100.0	29710	14	AY559091	SARS coro
41	21	100.0	29711	14	AY283794	SARS coro
42	21	100.0	29711	14	AY283796	SARS coro
43	21	100.0	29711	14	AY283798	SARS coro
44	21	100.0	29711	14	AY427439	SARS coro
45	21	100.0	29712	14	AY559093	SARS coro

ALIGNMENTS

RESULT 1	AY536760	1669 bp	mRNA	linear	VRL 15-SEP-2004
LOCUS	SARS coronavirus BJ01	nucleocapsid protein mRNA	complete cds.		
DEFINITION	AY536760				
ACCESSION	AY536760				
VERSION	AY536760.3	GI:52100973			
KEYWORDS	SARS coronavirus BJ01				
ORGANISM	SARS coronavirus BJ01				
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.				
AUTHORS	Li, T., Li, X., Chang, Z. and Liu, L.				
TITLE	Identification of SARS-CoV mRNA leader sequence				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1669)				
AUTHORS	Li, T., Li, X., Liu, L. and Chang, Z.				
TITLE	Direct Submission				
JOURNAL	Submitted (30-JAN-2004) Institute of Biomedicine, Tsinghua University, Beijing, Beijing 100084, China				
REFERENCE	3 (bases 1 to 1669)				
AUTHORS	Li, T., Li, X., Liu, L. and Chang, Z.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-JUL-2004) Institute of Biomedicine, Tsinghua University, Beijing, Beijing 100084, China				
REMARK	Sequence update by submitter				
REFERENCE	4 (bases 1 to 1669)				
AUTHORS	Li, T., Li, X., Chang, Z. and Liu, L.				
TITLE	Direct Submission				
JOURNAL	Submitted (15-SEP-2004) Institute of Biomedicine, Tsinghua University, Beijing 100084, China				
REMARK	Sequence update by submitter				
COMMENT	On Sep 15, 2004 this sequence version replaced gi:49921010.				
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	/country="China"				
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CDS					

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QLPGTTLPKGFYAGSRGSGOASRSSRSGNSRSTPGSSRGSNPARWASGGGT  
ALALLDLRLNKSQVSGQQOQGQVTVKSAEASKKPRKRTATKQYNVTQAFG  
RRGPEQTGNFGDQLIRQGYDHRWQIAQAFSAFFGMSRIGMEVTPSGTWLTY  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.62;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGACCACACAGGCAGATGG 21  
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Db 1359 ATGACCACACAGGCAGATGG 1379  
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RESULT 2

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AY534758S4 1873 bp RNA linear VRL 17-MAR-2004  
LOCUS SARS coronavirus Sin0409, partial sequence.  
DEFINITION  
ACCESSION AY534761  
VERSION AY534761.1 GI:45384968
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KEYWORDS

4 of 4

SOURCE

SARS coronavirus Sin0409

SARS coronavirus Sin0409

Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;

Coronaviridae; Coronavirus.

1 (bases 1 to 1873)

Lim,P.L., Kurup,A., Gopalakrishna,G., Chan,K.P., Wong,C.W.,

Ng,L.C., Se-Thoe,S.Y., Oon,L., Bai,X., Stanton,L.W., Ruan,Y.,

Miller,L.D., Vega,V.B., James,L., Ooi,P.L., Kai,C.S., Olsen,S.J.,

Ang,B. and Leo,Y.S.

Laboratory-acquired severe acute respiratory syndrome (SARS) -

Singapore 2003

Unpublished

2 (bases 1 to 1873)

Wei,C.L., Lee,C., Lin,S., Thoreau,H., Vega,V.B., Stanton,L.W. and

Ruan,Y.

Direct Submission

Submitted (28-JAN-2004) Genome Institute of Singapore, 60, Biopolis

Street, 02-01, Genome, Singapore 138672, Singapore

Location/Qualifiers

1..1873

/organism="SARS coronavirus Sin0409"

/mol_type="genomic RNA"

/db_xref="taxon:266147"

/country="Singapore"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.62;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1598 ATGACCACACAGGCAGATGG 1618  
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RESULT 3

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AY534762S6 1938 bp RNA linear VRL 17-MAR-2004  
LOCUS SARS coronavirus Sin_WNV, partial sequence.  
DEFINITION  
ACCESSION AY534767  
VERSION AY534767.1 GI:45384975
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KEYWORDS

6 of 6

SEGMENT

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SARS coronavirus Sin_WNV  
SARS coronavirus Sin_WNV  
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
Coronaviridae; Coronavirus.  
1 (bases 1 to 1938)  
Lim,P.L., Kurup,A., Gopalakrishna,G., Chan,K.P., Wong,C.W.,  
Ng,L.C., Se-Thoe,S.Y., Oon,L., Bai,X., Stanton,L.W., Ruan,Y.,  
Miller,L.D., Vega,V.B., James,L., Ooi,P.L., Kai,C.S., Olsen,S.J.,  
Ang,B. and Leo,Y.S.  
Laboratory-acquired severe acute respiratory syndrome (SARS) -  
Singapore 2003  
Unpublished  
2 (bases 1 to 1938)  
Wei,C.L., Lee,C., Lin,S., Thoreau,H., Vega,V.B., Stanton,L.W. and  
Ruan,Y.  
Direct Submission  
Submitted (28-JAN-2004) Genome Institute of Singapore, 60, Biopolis  
Street, 02-01, Genome, Singapore 138672, Singapore  
Location/Qualifiers  
1..1938  
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/country="Singapore"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.62;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1624 ATGACCACACAGGCAGATGG 1644  
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RESULT 4

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AY322205S4 2304 bp RNA linear VRL 21-JUL-2003  
LOCUS SARS coronavirus Shanghai LY Orf7a gene, partial cds; and Orf7b,  
DEFINITION Orf8a, Orf8b, and nucleocapsid protein genes, complete cds.  
ACCESSION AY322208  
VERSION AY322208.1 GI:32454342
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KEYWORDS

4 of 4

SARS coronavirus Shanghai LY

SARS coronavirus Shanghai LY

Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;

Coronaviridae; Coronavirus.

1 (bases 1 to 2304)

Yuan,Z., Zhang,X., Hu,Y., Lan,S., Wang,H., Zhou,Z. and Wen,Y.

Direct Submission

Submitted (12-JUN-2003) Molecular Virology, Shanghai Medical

College of Fudan University, 138 Yi Xue Yuan Road, Shanghai 200032,

P.R. China

Location/Qualifiers

1..2304

/organism="SARS coronavirus Shanghai LY"

/mol_type="genomic RNA"

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/country="China: Shanghai"

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/db_xref="GI:32454348"

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273..407

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/protein_id="AAP82971.1"

/db_xref="GI:32454349"

/translation="MNEILTIDFYLCFLAFLLVLVLMILFIWFSLIEQDLEEPCTKY

JOURNAL
TITLE
AUTHOR
DIRECT SUBMISSION
SUBMITTED (03-MAY-2003)
DEPARTMENT OF MICROBIOLOGY,
ZHEJIANG CENTER
OF TRANSLATION
/translation="MSDNGPQSNORASPRITFCGPTSDTNNNGRNGARPKORRRP
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ALALLLLDLNQLSKVSKCQCGQQTIVTKSAEASKKPRKRTATKQNVVTQAFG
ARGPEQTGNFGDQLIKQGDYIKHWPQIAQAFASAFFGMSRIGMEVTFSGTWLTY
HGATKLDDKDPQKDNVILNKHIDAYKTFFPTBPKKDKKKTDQAQPLPQKKQPT
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CDS

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Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 2486 ATGACCACACAGGCAGATGG 2506

RESULT 6
AY304489
LOCUS AY304489 8439 bp RNA linear VRL 05-NOV-2003
DEFINITION SARS coronavirus SZ1, partial genome.
ACCESSION AY304489
VERSION AY304489.1 GI:34482140

KEYWORDS
SOURCE SARS coronavirus SZ1
ORGANISM SARS coronavirus SZ1
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

REFERENCE 1 (bases 1 to 8439)
AUTHORS Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.

TITLE Isolation and characterization of viruses related to the SARS
coronavirus from animals in southern China
JOURNAL Science 302 (5643), 276-278 (2003)

MEDLINE 22913660
PUBMED 12958366
REFERENCE 2 (bases 1 to 8439)
AUTHORS Guan, Y. and Zheng, B.J.
TITLES Direct Submission
JOURNAL Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China

FEATURES
source
1..8439
/organism="SARS coronavirus SZ1"
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/db_xref="taxon:231516"
/country="Hong Kong"

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Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||

Db 8268 ATGACCACACAGGCAGATGG 8288

RESULT 7
AY304487
LOCUS AY304487 8581 bp RNA linear VRL 05-NOV-2003
DEFINITION SARS coronavirus SZ13, partial genome.
ACCESSION AY304487
VERSION AY304487.1 GI:34482138

KEYWORDS
SOURCE SARS coronavirus SZ13
ORGANISM SARS coronavirus SZ13
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

REFERENCE 1 (bases 1 to 8581)
AUTHORS Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.

TITLE Isolation and characterization of viruses related to the SARS
coronavirus from animals in southern China
JOURNAL Science 302 (5643), 276-278 (2003)

MEDLINE 22913660
PUBMED 12958366
REFERENCE 2 (bases 1 to 8581)
AUTHORS Guan, Y. and Zheng, B.J.
TITLES Direct Submission
JOURNAL Submitted (26-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China

FEATURES
source
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/country="Hong Kong"

ORIGIN
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGACCACACAGGCAGATGG 21
|||||

Db 8262 ATGACCACACAGGCAGATGG 8282

RESULT 8
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DEFINITION SARS coronavirus GZ60, partial genome.
ACCESSION AY304491
VERSION AY304491.1 GI:34482142

KEYWORDS
SOURCE SARS coronavirus GZ60
ORGANISM SARS coronavirus GZ60
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

REFERENCE 1 (bases 1 to 11006)
AUTHORS Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.

TITLE Isolation and characterization of viruses related to the SARS
coronavirus from animals in southern China
JOURNAL Science 302 (5643), 276-278 (2003)

MEDLINE 22913660
PUBMED 12958366
REFERENCE 2 (bases 1 to 11006)
AUTHORS Guan, Y. and Zheng, B.J.
TITLES Direct Submission
JOURNAL Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,

University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China

FEATURES

source
Location/Qualifiers
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/country="Hong Kong"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.69; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0

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Db 10669 ATGACCACACAGGCAGATGG 10689

RESULT 9

AY304493
LOCUS SARS coronavirus HKU-65806 linear VRL 05-NOV-2003
DEFINITION SARS coronavirus HKU-65806, partial genome.
ACCESSION AY304493
VERSION AY304493.1 GI:34482144

KEYWORDS

SARS coronavirus HKU-65806

SOURCE

SARS coronavirus HKU-65806
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

REFERENCE

1 (bases 1 to 11010)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.

Isolation and characterization of viruses related to the SARS

coronavirus from animals in southern China

Science 302 (5643), 276-278 (2003)

JOURNAL

MEDLINE 22913660

PUBMED 12958366

REFERENCE 2 (bases 1 to 11010)

Guan, Y. and Zheng, B.J.

Direct Submission

TITLE

Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,

University Pathology Building, Queen Mary Hospital, Pokfulam Road,

Hong Kong, China

FEATURES

source
Location/Qualifiers
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/isolate="HKU-65806"
/db_xref="taxon:231520"
/country="Hong Kong"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.69; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0

QY 1 ATGACCACACAGGCAGATGG 21

Db 10673 ATGACCACACAGGCAGATGG 10693

RESULT 10

AY304494
LOCUS SARS coronavirus HKU-66078 linear VRL 05-NOV-2003
DEFINITION SARS coronavirus HKU-66078, partial genome.
ACCESSION AY304494
VERSION AY304494.1 GI:34482145

KEYWORDS

SARS coronavirus HKU-66078

ORGANISM

SARS coronavirus HKU-66078
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

REFERENCE

1 (bases 1 to 11010)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.

Isolation and characterization of viruses related to the SARS

coronavirus from animals in southern China

Science 302 (5643), 276-278 (2003)

JOURNAL

MEDLINE 22913660

PUBMED 12958366

REFERENCE 2 (bases 1 to 11010)

Guan, Y. and Zheng, B.J.

Direct Submission

TITLE

Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,

University Pathology Building, Queen Mary Hospital, Pokfulam Road,

Hong Kong, China

FEATURES

source
Location/Qualifiers
1. .11010
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/mol_type="genomic RNA"
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/country="Hong Kong"

ORIGIN

Query Match 100.0%; Score 21; DB 14; Length 11010;
Best Local Similarity 100.0%; Pred. No. 0.69; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0

QY 1 ATGACCACACAGGCAGATGG 21

Db 10673 ATGACCACACAGGCAGATGG 10693

RESULT 11

AY304490
LOCUS SARS coronavirus GZ43, partial genome. linear VRL 05-NOV-2003
DEFINITION SARS coronavirus GZ43, partial genome.
ACCESSION AY304490
VERSION AY304490.1 GI:34482141

KEYWORDS

SARS coronavirus GZ43

SOURCE

SARS coronavirus GZ43
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

REFERENCE

1 (bases 1 to 13471)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.

Isolation and characterization of viruses related to the SARS

coronavirus from animals in southern China

Science 302 (5643), 276-278 (2003)

JOURNAL

MEDLINE 22913660

PUBMED 12958366

REFERENCE 2 (bases 1 to 13471)

Guan, Y. and Zheng, B.J.

Direct Submission

TITLE

Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,

University Pathology Building, Queen Mary Hospital, Pokfulam Road,

Hong Kong, China

FEATURES

source
Location/Qualifiers
1. .13471
/organism="SARS coronavirus GZ43"
/mol_type="genomic RNA"
/isolate="GZ43"
/db_xref="taxon:231517"
/country="Hong Kong"

ORIGIN

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 VMYASALMTWARTVADARRVMTLNVITLVYKYYGNALQDAISWALVISA
 TSNYSQVTTINFELARAVFVCEVYPLIFITGNTLQCLMLVFLGCGCCVFLGFC
 LTNVFRLLTGVYDVSTQEBFVYNSQGLPKPSIDAFKMLNICFKLGGKPKIVA
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 SEVLVKKKSLSEDEFDRAAMQKLEKADQAMTQMYKQARSDEKRAKTSAMQ
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 FYTASALRIQDQVADSKIVQISEINMDSNPLWPLIVTALRANSAAKLQNLSP
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 NSTVLSFCAVNDPAKAYDYLAGSQPIYNCVMKLTCTHTGCTQALITVPEANMDGS
 FGASCCLYCRCHIDHPNPKFCDLGKYVQIPTTCANDPVGFTVCTVCTGMMWKG
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 DWYDFVENPDLILRYANLGERVQSLLKTVOCDAMRDAGIVGLVTLNODLNGWYD
 FGDVQVAFCCGVPIVDSYVSLMPLTLITRALAASHMDADLAKPLIKWDLKDYFT
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 CONSRMT From independent foci of epidemic outbreak to large genomic
 TITLE alteration in late phase viruses: evolution of the SARS-coronavirus
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 29350)
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